

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 07:43:47 ; Search time 11596 Seconds

(without alignments)  
11459.964 Million cell updates/sec

Title: US-09-719-485-1

Perfect score: 3066  
Sequence: 1 ttgaattatctgtcactg.....acgtgaagacgatggataa 3066

Scoring table:

IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_da:\*

2: gb\_hg:\*

3: gb\_in:\*

4: gb\_cm:\*

5: gb\_ov:\*

6: gb\_ph:\*

7: gb\_pl:\*

8: gb\_pr:\*

9: gb\_ro:\*

10: gb\_sy:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_un:\*

15: gb\_un:\*

16: em\_hum:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_mu:\*

21: em\_or:\*

22: em\_or:\*

23: em\_or:\*

24: em\_or:\*

25: em\_or:\*

26: em\_or:\*

27: em\_or:\*

28: em\_or:\*

29: em\_or:\*

30: em\_or:\*

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32: em\_or:\*

33: em\_or:\*

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35: em\_or:\*

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40: em\_or:\*

41: em\_or:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	3050.8	99.5	349880	6	AX711879	AX711879 Sequence
5	3050.8	99.5	349880	6	AX739961	AX739961 Sequence
6	2026	66.1	2040	9	AF034632	AF034632 Homo sapi
7	1038	33.9	1161	6	AX154591	AX154591 Sequence
8	1038	33.9	1390	6	BD211244	BD211244 Cloning a
9	901	29.4	1239	6	AX154589	AX154589 Sequence
10	901	29.4	1239	6	AX549187	AX549187 Sequence
11	901	29.4	1239	6	AX572865	AX572865 Sequence
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15	591.2	19.3	692	9	HSB342408	AJ342408 Homo sapi
16	576.4	18.8	615	9	HSB339459	AJ339459 Homo sapi
17	550.6	18.0	674	9	HSB330081	AJ330081 Homo sapi
18	487.8	15.9	703	9	HSB340216	AJ340216 Homo sapi
19	480.4	15.6	742	9	HSB340035	AJ340035 Homo sapi
20	478.6	15.7	807	9	HSB337736	AJ337736 Homo sapi
21	444.8	14.5	746	9	HSB341117	AJ341117 Homo sapi
22	443.8	14.5	701	9	HSB326768	AJ326768 Homo sapi
23	414.4	13.5	749	9	HSB323055	AJ323055 Homo sapi
24	411	13.4	693	9	HSB340953	AJ340953 Homo sapi
25	404.4	13.2	722	9	HSB340215	AJ340215 Homo sapi
26	402	13.1	681	9	HSB341310	AJ341310 Homo sapi
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33	283	9.2	283	6	AR303910	AR303910 Sequence
34	283	9.2	283	6	BD056681	BD056681 Galania r
35	283	9.2	283	6	BD064652	BD064652 Human gal
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42	248.2	8.1	1050	6	BD222611	BD222611 Canine gr
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45	233.2	7.6	870	4	SSU60180	U60180 Sus scrofa

ALIGNMENTS

RESULT 1

BD211242

LOCUS

BD211242

DEFINITION

Cloning and identification of motilin receptor.

ACCESSION

BD211242

VERSION

BD211242.1 GI:33021012

KEYWORDS

JP 2002517507-A/1.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 3066)

Feiguer, S.D., Patchett, A.A., Tan, C., McKee, K., Macneil, D., Howard, A.D., Peng, S.S. and Smith, R.G.

Cloning and identification of motilin receptor

TITLE

JOURNAL Patent: JP 2002517507-A 1 18-JUN-2002;  
 MERCK AND CO INC  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002517507-A/1  
 PD 18-JUN-2002  
 PF 08-JUN-1999 JP 2000553444  
 PR 12-JUN-1998 US 60/088098  
 PI SCOTT D FEIGENBER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI  
 DOUGLAS MACNELL,  
 PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH  
 PC C07K14/705, A61K38/00, A61P1/00, C12N15/09, C1201/02, A61K37/02, PC  
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 Location/Qualifiers  
 FT source 1..3066  
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ORIGIN

Query Match 100.0%; Score 3066; DB 6; Length 3066;  
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 Matches 3066; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GAGGTCGAGCGGGTGGACCACTGGGGTCAGAGTTCCAGACCAAGCTGACCATGG 120
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DB 721 GGGTATTCAGATTAGTGAAGAGGAAAGGCGCCCTGGAAGTGTATGGGCGCGGAGAGGCG 780
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RESULT 2  
 AL137000  
 LOCUS  
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 Human DNA sequence from clone RP11-203116 on chromosome 13 contains the gene for KIA0970 protein, COX7C1 (cytochrome c oxidase subunit VIIC pseudogene 1), a novel pseudogene, the GPR38 (G protein-coupled receptor 38) gene, ESTs, STSs, GSSs and a CpG island, complete sequence.  
 AL137000  
 VERSION  
 AL137000.6 GI:9944121  
 HTG: COX7C1, CpG island, cytochrome c oxidase, G protein-coupled receptor, GPR38, KIA0970.  
 KEYWORDS  
 Homo sapiens (human)  
 SOURCE  
 Homo sapiens  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 (bases 1 to 163284)  
 Wall, M.  
 Direct Submission  
 Submitted (18-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 JOURNAL  
 requests: clonerequest@sanger.ac.uk  
 COMMENT  
 On Aug 29, 2000 this sequence version replaced gi:9926419.  
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  
 Bm: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMBSP; Information on the WORMBSP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormp  
 This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr13  
 IMPORTANT: This sequence is not the entire insert of clone RP11-203116. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.  
 The true left end of clone RP11-452110 is at 1 in this sequence. The true right end of clone RP11-103318 is at 163284 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-203116 is from the library RPI1-11.1 constructed by the group of Plesier de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: pBAC3.6.

FEATURES  
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 /mol\_type="genomic DNA"





Query Match 99.5%; Score 3050.8; DB 9; Length 163284;  
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REFERENCE 1  
AUTHORS Zhang, Y., Moffatt, M. and Cookson, W.  
TITLE Treatment and diagnosis of B cell chronic lymphocytic leukaemia  
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ORIGIN

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QY 2459 TGCCAGAGCGGCTGTTCAAGAAATTGCTCTCTGCTTAAAGTATTCAGAGCTGATPACA 2518

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AF034632 2040 bp DNA linear PRI 13-JUL-1998

LOCUS AF034632

DEFINITION Homo sapiens orphan G protein-coupled receptor (GPR38) gene,

ACCESSION AF034632

VERSION AF034632.1 GI:2654158

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

1 (bases 1 to 2040)

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,

Hreniuk,D.L., Smith,R.G., Howard,A.D., and Van der Pleeg,L.H.

Cloning and characterization of two human G protein-coupled

receptor genes (GPR38 and GPR39) related to the growth hormone

secretagogue and neuropeptin receptors

Genomics 46 (3), 426-434 (1997)

JOURNAL

MEDLINE

PUBMED

9441746

98110578

2 (bases 1 to 2040)

McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,

Hreniuk,D.L., Smith,R.G., Van der Pleeg,L.H.T. and Howard,A.D.

Direct Submission

Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co.,

Inc., PO Box 2000, Rahway, NJ 07065, USA

location/Qualifiers

FEATURES

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Query Match 66.1%; Score 2026; DB 9; Length 2040;  
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RESULT 7  
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LOCUS AX154591  
DEFINITION Sequence 11 from Patent WO0138355.  
ACCESSION AX154591  
VERSION AX154591.1 GI:14536177  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
Shepard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D.  
Method of forming a peptide-receptor complex with zsig3 and  
therapeutic use thereof  
Patent: WO 0138355-A 11 31-MAY-2001;  
JOURNAL Zymogenetics, Inc. (US)  
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Query Match 33.9%; Score 1038; DB 6; Length 1161;  
Best Local Similarity 99.8%; Pred. No. 4.4e-153;  
Matches 1050; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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RESULT 8  
BD211244 1390 bp DNA linear PAT 17-JUL-2003  
LOCUS BD211244  
DEFINITION Cloning and identification of motilin receptor.  
ACCESSION BD211244  
VERSION BD211244.1 GI:33021014  
KEYWORDS JP 2002517507-A/3.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1390)  
Feighner, S.D., Patchett, A.A., Tan, C., McKee, K., Macneil, D.,  
Howard, A.D., Pong, S.S. and Smith, R.G.  
Cloning and identification of motilin receptor  
Patent: JP 2002517507-A 3 18-JUN-2002;  
MERCK AND CO INC  
OS Homo sapiens (human)  
PN JP 2002517507-A/3  
PD 18-JUN-2002  
PF 08-JUN-1999 JP 2000553444  
PI 12-JUN-1998 US 60/089098  
PI SCOTT D FEIGNER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI  
DOUGLAS MACNEIL,  
PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH  
PC C07K14/705, A61K38/00, A61P1/00, C12N15/09, C12Q1/02, A61K37/02, PC  
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FT source

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Best Local Similarity	99.8%;	Pred. No. 4.4e-153;		
Matches 1050; Conservative	0;	Mismatches	0;	Indels 2; Gaps 1

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ACCESSION	AX154589				
VERSION	AX154589.1	GI:14536175			
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REFERENCE		1			
AUTHORS		Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D.			
TITLE		Method of forming a peptide-receptor complex with zsig33 and therapeutic use thereof			
JOURNAL		Patent: WO 0138355-A 9 31-MAY-2001; Zymogenetics, Inc. (US)			
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QY 1449 TGCAGCCGCTCGCGCGCGCGCTGTCACCGCGCGCGCTCGCGCGCTCATGCT 1508  
DB 421 TGCAGCCGCTCGCGCGCGCGCTGTCACCGCGCGCGCTCGCGCGCTCATGCT 480  
QY 1509 GTGCTCTGGGCGCGTGGGCGGCTCTGCGCGGTCCTCTTGTTCCTGGTGGGCGTGGAG 1568  
DB 481 GTGCTCTGGGCGCGTGGGCGGCTCTGCGCGGTCCTCTTGTTCCTGGTGGGCGTGGAG 540  
QY 1569 CAGGACCCCGGCACTTCCTGATGTCGCGGCTCATGAGCAACCGCGGATTCGCTCTCG 1628  
DB 541 CAGGACCCCGGCACTTCCTGATGTCGCGGCTCATGAGCAACCGCGGATTCGCTCTCG 600  
QY 1629 CTTCTGCGCTGTGTGGCGGCTCTTGTGCTCTGCGCGCGCGCAACCGCGCTCGCGCTG 1688  
DB 601 CTTCTGCGCTGTGTGGCGGCTCTTGTGCTCTGCGCGCGCGCAACCGCGCTCGCGCTG 660  
QY 1689 GGGCCCGAGACCGGCGGAGCGCGCGCTGTCAGCGCGGATGCGGCGGAGCCCGCG 1748  
DB 661 GGGCCCGAGACCGGCGGAGCGCGCGCTGTCAGCGCGGATGCGGCGGAGCCCGCG 720  
QY 1749 CAGCTGGGCGCGCTGCTGTGATGCTGTGGGTACACCGCGCTACTTTCTTCTGCTCTT 1808  
DB 721 CAGCTGGGCGCGCTGCTGTGATGCTGTGGGTACACCGCGCTACTTTCTTCTGCTCTT 780  
QY 1809 CTGTGCTCTGACATCTCTACGGGCTCATGCGGCGGAGCTGTGAGAGACCGCGCGCG 1868  
DB 781 CTGTGCTCTGACATCTCTACGGGCTCATGCGGCGGAGCTGTGAGAGACCGCGCGCG 840  
QY 1869 CTGCGAGGCGCGCGCGCTCTGCGGCGGAGAGAGCGGACCGGCGGAGCGGTCCGCTCTG 1928  
DB 841 CTGCGAGGCGCGCGCGCTCTGCGGCGGAGAGAGCGGACCGGCGGAGCGGTCCGCTCTG 900  
QY 1929 C 1929  
DB 901 C 901

RESULT 10  
AX549187 1239 bp DNA linear PAT 26-NOV-2002  
LOCUS AX549187  
DEFINITION Sequence 472 from Patent WO02061087.  
ACCESSION AX549187  
VERSION AX549187.1 GI:25813904  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Burmer, G.C., Roush, C.L. and Brown, V.P.  
Antigenic peptides, such as for G protein-coupled receptors  
(GPCR), antibodies thereto, and systems for identifying such  
antigenic peptides  
Patent: WO 02061087-A 472 08-AUG-2002;  
Lifespan Biosciences, Inc. (US)  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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Query Match 29.4%; Score 901; DB 6; Length 1239;  
Best local Similarity 100.0%; Pred. No. 1.3e-131;

Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 ATGGGAGCCCTTGGAGACGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60  
QY 1089 GGGCGCGCGCTTGGAGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1148  
DB 61 GGGCGCGCGCTTGGAGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
QY 1149 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1208  
DB 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
QY 1209 ATGCTGATCGGCGGCTTACCGGAGCATGCGGACCAACCACTTGTACTTGGGCGAGCATG 1268  
DB 181 ATGCTGATCGGCGGCTTACCGGAGCATGCGGACCAACCACTTGTACTTGGGCGAGCATG 240  
QY 1269 GCGGCTGCGGAGCTTACTGATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1328  
DB 241 GCGGCTGCGGAGCTTACTGATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 300  
QY 1329 TCGCGGCGCTGGGTTTGGGCGCGCTGCTGTGCGGCTGTGCTGTGCTGTGCTGTGCTGTG 1388  
DB 301 TCGCGGCGCTGGGTTTGGGCGCGCTGCTGTGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 360  
QY 1389 TGCACCTACGCGACGCTGTGATGTCGCGGCTCATGAGCAACCGCGGATTCGCTCTCG 1448  
DB 361 TGCACCTACGCGACGCTGTGATGTCGCGGCTCATGAGCAACCGCGGATTCGCTCTCG 420  
QY 1449 TGCAGCCGCTCGCGCGCGCGCTGTCACCGCGCGCGCTCGCGCGCTCATGCT 1508  
DB 421 TGCAGCCGCTCGCGCGCGCGCTGTCACCGCGCGCGCTCGCGCGCTCATGCT 480  
QY 1509 GTGCTCTGGGCGCGTGGGCGGCTCTGCGCGGTCCTCTTGTTCCTGGTGGGCGTGGAG 1568  
DB 481 GTGCTCTGGGCGCGTGGGCGGCTCTGCGCGGTCCTCTTGTTCCTGGTGGGCGTGGAG 540  
QY 1569 CAGGACCCCGGCACTTCCTGATGTCGCGGCTCATGAGCAACCGCGGATTCGCTCTCG 1628  
DB 541 CAGGACCCCGGCACTTCCTGATGTCGCGGCTCATGAGCAACCGCGGATTCGCTCTCG 600  
QY 1629 CTTCTGCGCTGTGTGGCGGCTCTTGTGCTCTGCGCGCGCGCAACCGCGCTCGCGCTG 1688  
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QY 1749 CAGCTGGGCGCGCTGCTGTGATGCTGTGGGTACACCGCGCTACTTTCTTCTGCTCTT 1808  
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DB 781 CTGTGCTCTGACATCTCTACGGGCTCATGCGGCGGAGCTGTGAGAGACCGCGCGCG 840  
QY 1869 CTGCGAGGCGCGCGCGCTCTGCGGCGGAGAGAGCGGACCGGCGGAGCGGTCCGCTCTG 1928  
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QY 1929 C 1929  
DB 901 C 901

RESULT 11  
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LOCUS AX572965  
DEFINITION Sequence 1 from Patent WO02057791.  
ACCESSION AX572965  
VERSION AX572965.1 GI:26005013

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Db	781	CTGGGCTTCACATCTCTCTTACGGGCTCTATTCGGGCGGGAGCGTGTGAGACGCGCGGCGG	840
QY	1869	CTGGGAGGCGCGGCGCTCTCGGGGCGGGAGAGAGGCCACCTGGACAGCCGTCGCTCTG	1928
Db	841	CTGGGAGGCGCGGCGCTCTCGGGGCGGGAGAGAGGCCACCTGGACAGCCGTCGCTCTG	900
QY	1929	C 1929	
Db	901	C 901	
RESULT 12			
LOCUS	BD211243	1239 bp	DNA linear PAT 17-JUL-2003
DEFINITION	Cloning and identification of motilin receptor.		
ACCESSION	BD211243		
VERSION	BD211243.1	GI:33021013	
KEYWORDS	JP 2002517507-A/2.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (Bases 1 to 1239) Feighner,S.D., Patchett,A.A., Tan,C., McKee,K., Macnei,D., Howard,A.D., Pong,S.S. and Smith,R.G.		
TITLE	Cloning and identification of motilin receptor		
JOURNAL	Patent: JP 2002517507-A 2 18-JUN-2002; MERCK AND CO INC		
COMMENT	OS Homo sapiens (human) PN JP 2002517507-A/2 PD 18-JUN-2002 PF 08-JUN-1999 JP 2000553444 PR 12-JUN-1998 US 60/089098 PI SCOTT D FEIGHNER,ARTHUR A PATCHETT,CARINA TAN,KAREN MCKEE, PI DOUGLAS MACNEIL, PI ANDREW D HOWARD,SHENG SHUNG PONG,ROY G SMITH PC C071314/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC C12N15/00 CC Cloning and identification of motilin receptor. FH Key Location/Qualifiers FT source 1..1239 FT Location/Qualifiers 1..1239 /organism='Homo sapiens (human)'. /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'		
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Best Local Similarity	100.0%; Pred. No. 1,3e-131; Indels 0; Gaps 0;		
Matches	901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	1	ATGGGCAAGCCCTTGTGAACGAGCAGCGCCCGAGGGGCGCGGAGCCGCTGGGCC	60
QY	1089	GCGGTGCGCGCTTGTGCGAGAGCGCGGTGCTCCCTTCCCTGGGGGGGCTGTGTCGCG	1148
Db	61	GCGGTGCGCGCTTGTGCGAGAGCGCGGTGCTCCCTTCCCTGGGGGGGCTGTGTCGCG	120
QY	1149	GTCAGCGCTGTGTGCTGTGCTGTGTCGTGTCGTGGGGGTGAGCGGCAAGTGTGACCGTG	1208
Db	121	GTCAGCGCTGTGTGCTGTGCTGTGTCGTGTCGTGGGGGTGAGCGGCAAGTGTGACCGTG	180
QY	1209	ATGCTGATGCGGGGCTTACCGGGGACATCGGAGACCAACCAACTGTGTCCTGGGAGCATG	1268
Db	181	ATGCTGATGCGGGGCTTACCGGGGACATCGGAGACCAACCAACTGTGTCCTGGGAGCATG	240
QY	1269	GCGGTGCGCACTACTCATCTGCTCGGGCTGCGCTTGACCTGTACCGCTCTGGCGC	1328

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Db      241  GCGCTGTCGACCTACTCATCTGCTGCGGCGTGGCCCTTGACCTGTACCCGCTCTGAGCG 300
Qy      1329  TCGGCGGCGCTGAGGCTTCGCGGCGCGCGCTGCTGCGCGCTGCTGCTACACGCGGCGAGAGCG 1388
Db      301  TCGGCGGCGCTGAGGCTTCGCGGCGCGCGCTGCTGCGCGCTGCTGCTACACGCGGCGAGAGCG 360
Qy      1389  TGCACCTACGCAACGCTGCTGCAATGACCGCGCTGACGCTGAGCGCTACCTGAGCCATC 1448
Db      361  TGCACCTACGCAACGCTGCTGCAATGACCGCGCTGACGCTGAGCGCTACCTGAGCCATC 420
Qy      1449  TGCCTGCGGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1508
Db      421  TGCCTGCGGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy      1509  GTGCTGCGGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1568
Db      481  GTGCTGCGGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy      1569  CAGACCCCGGCGCATCTCCGTAAGTCCGAGGCTCAATGACCGCGCGGATGCGCTCTCTG 1628
Db      541  CAGACCCCGGCGCATCTCCGTAAGTCCGAGGCTCAATGACCGCGCGGATGCGCTCTCTG 600
Qy      1629  CCTTCCGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1688
Db      601  CCTTCCGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Qy      1689  GGGCCCGAGACCGCGGAGCGCGCGCGCTGTTACGCGCGAATGCGCGCGCGAGCGCGCG 1748
Db      661  GGGCCCGAGACCGCGGAGCGCGCGCGCTGTTACGCGCGAATGCGCGCGCGAGCGCGCG 720
Qy      1749  CAGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1808
Db      721  CAGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy      1809  CTGCTGCTGACATCTCTACGCGGCTCATGCGCGGAGCTGTGAGACGACGCGCGAGCG 1868
Db      781  CTGCTGCTGACATCTCTACGCGGCTCATGCGCGGAGCTGTGAGACGACGCGCGAGCG 840
Qy      1869  CTGCGAGCGCGCGCGCTGCGCGCGGAGAGAGGCGCACCGGCAACCGCTGCGCGCTGCTG 1928
Db      841  CTGCGAGCGCGCGCGCTGCGCGCGGAGAGAGGCGCACCGGCAACCGCTGCGCGCTGCTG 900
Qy      1929  C 1929
Db      901  C 901

RESULT 13
BD211249 900 bp DNA linear PAT 17-JUL-2003
LOCUS Cloning and identification of molilin receptor.
ACCESSION BD211249
VERSION BD211249.1 GI:33021019
KEYWORDS JP 2002517507-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS Feighner,S.D., Patchett,A.A., Tan,C., McKee,K., Macneil,D.,
Howard,A.D., Pong,S.S. and Smith,R.G.
TITLE Cloning and identification of molilin receptor
JOURNAL Patent: JP 2002517507-A 8 18-JUN-2002;
MERCK AND CO INC
COMMENT OS Homo sapiens (human)
PN JP 2002517507-A/8
PD 18-JUN-2002
PF 08-JUN-1999 JP 200053444
PI 12-JUN-1998 US 60/089098
PI SCOTT D FEIGNER,ARTHUR A PATCHETT,CARINA TAN,KAREN MCKEE, PI
DOUGLAS MACNEIL,
PI ANDREW D HOWARD,SHENG SHING PONG,ROY G SMITH

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PC C07K14/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC
C12N15/00
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FT source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.9e-131;
Matches 900; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1089 GCGTGCAGCGCTTGGAGAGAGCGCGCTGCTGCGCTTCCCTGAGGAGCGCTGAGCGG 1148
Db 61 GCGTGCAGCGCTTGGAGAGAGCGCGCTGCTGCGCTTCCCTGAGGAGCGCTGAGCGG 120
Qy 1149 GTGACCGCTGTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208
Db 121 GTGACCGCTGTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy 1209 ATGCTGATGAGGCGGTACCGGAGCAATGCGACCAACCACTGTATCTTGGAGCATG 1268
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Db 721 CAGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 1809 CTGCTGCTGACATCTCTACGCGGCTCATGCGCGGAGCTGTGAGACGACGCGCGAGCGG 1868
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[illegible]

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VERSION	AJ342408							
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SOURCE	Homo sapiens (human)							
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
REFERENCE	Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M., Podewski,I.R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Lovelache,V.G., Kolchanov,N.A., Protodopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlstedt,C. and Zharovsky,E.R. NotI flanking sequences: a tool for gene discovery and verification of the human genome							
TITLE	Nucleic Acids Res. 30 (14), 3163-3170 (2002)							
JOURNAL	MEDLINE 22131767							
PUBMED	12136098							
REFERENCE	2 (bases 1 to 692)							
AUTHORS	Zabarovskiy,E.R.							
TITLE	Direct Submission							
JOURNAL	Submitted (16-MAY-2001) Microbiology and Tumorphiology Centre, Karolinska Institute, Theorells vag, 3, box 280, Stockholm 171 77, Sweden							
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Best Local Similarity 91.8%; Pred.No. 5e-83;								
Matches 635; Conservative 0; Mismatches 55; Indels 2; Gaps 1;								
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Db	1	GGCGCGCGGAGACACCAATGGCACCCCTGGAAGGAGAGAGCGCCCGAGGAGGCG	60					
OY	1070	GGCGGACCGCGGTGCGCCCGCTGCGCGCTTGGAGAGAGCGCGCTGCGCCCTTTC	1129					
Db	61	GGCGGACCGCGGTGCGCCCGCTGCGCGCTTGGAGAGAGCGCGCGCTGCGCCCTTTC	120					
OY	1130	CTTGGGGGCGCTGTGCTCCGCTGACCGCTGTGTGCTGTGCTGTTCCTGTCTGCGGGTGA	1189					
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Db 181 CGGCAAGGTGGTGAACCGGATGATGCGGCGCTACCGGAGCATGGCGACATCAACCA 240
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

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Minimum DB seq length: 0

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Maximum Match 100%  
Listing first 45 summaries

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22	248.2	8.1	1050	3	AAZ61492
23	234.8	7.7	1063	2	AAI69754

24	234.8	7.7	1063	2	AAI68662	AAI68662 Pig growt
25	233.2	7.6	1029	2	AAI69755	AAI69755 Swine gro
26	233.2	7.6	1029	2	AAI68663	AAI68663 Pig growt
27	231.6	7.6	1095	3	AAZ45993	AAZ45993 CDNA enco
28	231.6	7.6	4009	3	AAZ45967	AAZ45967 DNA enco
29	229	7.5	250	7	ACA55761	ACA55761 Pig signa
30	228.8	7.5	870	7	ABZ42674	ABZ42674 Human gro
31	228.8	7.5	1122	2	AAI68665	AAI68665 Human gro
32	228.4	7.4	1092	4	AAI27800	AAI27800 Rat growt
33	228.4	7.4	3129	2	AAI69759	AAI69759 Rat growt
34	228.4	7.4	3129	2	AAI68667	AAI68667 Rat growt
35	227.8	7.4	1088	2	AAI69756	AAI69756 Human gro
36	227.8	7.4	1088	2	AAI68664	AAI68664 Human gro
37	227.8	7.4	1101	3	AAZ51463	AAZ51463 Human G P
38	227.8	7.4	1101	3	AAA30732	AAA30732 DNA enco
39	227.8	7.4	1101	3	AAA30643	AAA30643 Human G P
40	227.8	7.4	1101	4	AAI63680	AAI63680 Human G-P
41	227.8	7.4	1101	6	AAI630395	AAI630395 Human gro
42	227.8	7.4	1101	7	ACA55650	ACA55650 Human gro
43	227.8	7.4	1101	9	ADC22606	ADC22606 Human G P
44	227.8	7.4	1101	9	ADC22728	ADC22728 Human G P
45	227.8	7.4	1101	10	ADD35397	ADD35397 Human gro

## ALIGNMENTS

RESULT 1	AAZ45402	standard; DNA; 3066 BP.
ID	AAZ45402	
XX	AAZ45402;	
AC	AAZ45402;	
XX	AAZ45402;	
DT	27-MAR-2000	(first entry)
XX	27-MAR-2000	
DE	Genomic sequence of the motilin receptor gene including 5' UTR.	
XX	Genomic sequence of the motilin receptor gene including 5' UTR.	
KW	Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;	
KW	spliced form; MTL-R1a; MTL-R1b; gastric motility disorder;	
KW	functional defect; neurological disorder; scleroderma; colonoscopy;	
KW	paraneoplastic syndrome; radiation induced dysmotility; diabetes;	
KW	infection; stress-related motility disorder; psychogenic disorder;	
KW	gastropareisis; gastro-oesophageal reflux disease; constipation;	
KW	chronic idiopathic pseudo obstruction; acute faecal impaction;	
KW	postoperative ileus; gallstones; infantile colic; diarrhoea;	
KW	irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;	
KW	endoscopy; duodenal intubation; ds.	
OS	Homo sapiens.	
XX	Homo sapiens.	
XX	Homo sapiens.	
FX	Key	Location/Qualifiers
FT	misc_feature	1929..1931
FT	misc_feature	/tag= a
FT	misc_feature	/note= "imperfect donor site"
FT	intron	1930..2728
FT	intron	/tag= b
FT	misc_feature	/note= "intronic sequence"
FT	misc_feature	2080..2082
FT	misc_feature	/tag= c
FT	misc_feature	/note= "perfect donor site"
FT	misc_feature	2729..2732
FT	misc_feature	/tag= d
FT	misc_feature	/note= "perfect splice acceptor site"
XX	W09964436-A1.	
XX	16-DEC-1999.	
XX	16-DEC-1999.	
PF	08-JUN-1999;	99WO-USO12773.
XX	08-JUN-1999;	
PR	12-JUN-1998;	98US-0089058P.
XX	12-JUN-1998;	
PA	(MERI ) MERCK & CO INC.	

QY	TTGAAATTATCTGGTCACTCCGGGCGCGGTGGCTACACGCTGTAATCCAGACATTGG	60
Db	1 TTGAATTTATCTGGTCACTCCGGGCGCGGTGGCTACACGCTGTAATCCAGACATTGG	60
QY	61 GAGGTGAGGCGGGTGGACCACTTGAGGTTCAGACACAGGCTGGCCAAATGG	120
Db	61 GAGGTGAGGCGGGTGGACCACTTGAGGTTCAGACACAGGCTGGCCAAATGG	120
QY	121 CGAAACCCCTGATCACCAAAAAACAAAAATTTAGCGCGGGGCTGTGGGGGCTCTGTGTC	180
Db	121 CGAAACCCCTGATCACCAAAAAACAAAAATTTAGCGCGGGGCTGTGGGGGCTCTGTGTC	180
QY	181 CCAGCTACTGAGGAGGCTGAGGTGGGAGGACTGTGAACCTGGGAGGTCGAGGCTGGAG	240
Db	181 CCAGCTACTGAGGAGGCTGAGGTGGGAGGACTGTGAACCTGGGAGGTCGAGGCTGGAG	240
QY	241 TGAAGCTGATCGCGCACTTAAACTTCAGCTGACGACAGTGAACCTGTCTCAAGA	300
Db	241 TGAAGCTGATCGCGCACTTAAACTTCAGCTGACGACAGTGAACCTGTCTCAAGA	300
QY	301 AGAAAAAAGAAAAAGAAAGAAAAAAGAAAAAAGAAAAAAGAAAAATTTTGGTCAATTAAT	360
Db	301 AGAAAAAAGAAAAAGAAAGAAAAAAGAAAAAAGAAAAAAGAAAAATTTTGGTCAATTAAT	360
QY	361 GGTGAGCTCCCTCCACCACTCGCGAATTTTACAGAAAGAGAACTGGGCTGGGCGAGACC	420
Db	361 GGTGAGCTCCCTCCACCACTCGCGAATTTTACAGAAAGAGAACTGGGCTGGGCGAGACC	420
QY	421 AGGACTAGCCCAAGATTACCAAGTTACTCGGTTGTAGGCCAGGATTAGACAGAGAGG	480
Db	421 AGGACTAGCCCAAGATTACCAAGTTACTCGGTTGTAGGCCAGGATTAGACAGAGAGG	480
QY	481 CTCTAGATTCTGGTCTTGAATCCCTCTCTATTATTAGCATTAATGGCTTCTGAGAGATTA	540
Db	481 CTCTAGATTCTGGTCTTGAATCCCTCTCTATTATTAGCATTAATGGCTTCTGAGAGATTA	540
QY	541 CCATGAGCCCTCCACCGTCAAGGGGAGGACGACGACCAAGACAGATCCTTTCGA	600
Db	541 CCATGAGCCCTCCACCGTCAAGGGGAGGACGACGACCAAGACAGATCCTTTCGA	600

QY	601	AGGAGCCCGGAGTACCAAGACTGACCAAAAGGCCGTACAGTGCTCACTCTGTAAACAA	660
Db	601	AGGAGCCCGGAGTACCAAGACTGACCAAAAGGCCGTACAGTGCTCACTCTGTAAACAA	660
QY	661	GCTGTCTTAGGGTGGACATATGCTCACCAGACCCGGGTAAAGGCTCTGTACGAGCGCC	720
Db	661	GCTGTCTTAGGGTGGACATATGCTCACCAGACCCGGGTAAAGGCTCTGTACGAGCGCC	720
QY	721	GGGTATTCACATTAGTGTAGAGAGGAGCGCCCTTGAACTGTATGGAGCCCGGAGAGCGC	780
Db	721	GGGTATTCACATTAGTGTAGAGAGGAGCGCCCTTGAACTGTATGGAGCCCGGAGAGCGC	780
QY	781	CGGAGAGCGAGACATATGGCCCGGGCCCGGGCCCGGCCCGGTGGGCGGAGACTGGCGCCAG	840
Db	781	CGGAGAGCGAGACATATGGCCCGGGCCCGGGCCCGGCCCGGTGGGCGGAGACTGGCGCCAG	840
QY	841	CTAGCTCGGAGAGCGCTTCGAGAGCCACCCCGCAGAGCCGCTTCTCGCGCCCCGAGCGCA	900
Db	841	CTAGCTCGGAGAGCGCTTCGAGAGCCACCCCGCAGAGCCGCTTCTCGCGCCCCGAGCGCA	900
QY	901	CGCGAGCGCTCCCGCGCTCTGACCTGGCCGCGCCGACGTCGCGGGCTGGGAAAGAGCGC	960
Db	901	CGCGAGCGCTCCCGCGCTCTGACCTGGCCGCGCCGACGTCGCGGGCTGGGAAAGAGCGC	960
QY	961	CTCACCGAGAGGAGCAACGCGCCAGGCTCCAGCCGACCCGAGACGCGCGCCCGCGC	1020
Db	961	CTCACCGAGAGGAGCAACGCGCCAGGCTCCAGCCGACCCGAGACGCGCGCCCGCGC	1020
QY	1021	GAGCACCCATGGGAGAGCCCTTGAAACGCGACGACGAGCCCGGAGAGGAGCGCGGAGCGC	1080
Db	1021	GAGCACCCATGGGAGAGCCCTTGAAACGCGACGAGCCCGGAGAGGAGCGCGGAGCGC	1080
QY	1081	CGTGGCCCGCGCTCCGCGCTTGCAGACGACGCGCTGTGCGCCCTTCCCTGGGGGCGC	1140
Db	1081	CGTGGCCCGCGCTCCGCGCTTGCAGACGACGCGCTGTGCGCCCTTCCCTGGGGGCGC	1140
QY	1141	TGGTGGCCGCTAACCGCTGTGTGCGCTGTGACCTGTTGATGTGGGGGTGAGCGGCAACGTGG	1200
Db	1141	TGGTGGCCGCTAACCGCTGTGTGCGCTGTGACCTGTTGATGTGGGGGTGAGCGGCAACGTGG	1200
QY	1201	TGACCGGTATGCTGATCGGAGCGCTAACCGGAGCATGCGGACCAACCACTTGTATCTTGG	1260
Db	1201	TGACCGGTATGCTGATCGGAGCGCTAACCGGAGCATGCGGACCAACCACTTGTATCTTGG	1260
QY	1261	GCAGATAGGCGGTGTCCGACCTTACATCTGCTGTGCGGCTGTGACCTGTATACCGCC	1320
Db	1261	GCAGATAGGCGGTGTCCGACCTTACATCTGCTGTGCGGCTGTGACCTGTATACCGCC	1320
QY	1321	TCTGGCGCTCGCGGCCCTGGGTGTTCGGGGCGCTGTCTGTCGCGCTGTCTCTTACGTGG	1380
Db	1321	TCTGGCGCTCGCGGCCCTGGGTGTTCGGGGCGCTGTCTGTCGCGCTGTCTCTTACGTGG	1380
QY	1381	GCGAGGGGTGACCTGACCGGCAACGCTGTGACATGACCGGCTGTGACCGCTGTGACCGGCTGAC	1440
Db	1381	GCGAGGGGTGACCTGACCGGCAACGCTGTGACATGACCGGCTGTGACCGGCTGTGACCGGCTGAC	1440
QY	1441	TGGCCATCTGCGCGCCGCTCCGCGCCGCGCGTCTTGTGTACCCCGGCGCGCGCTCCGCGCGC	1500
Db	1441	TGGCCATCTGCGCGCCGCTCCGCGCCGCGCGTCTTGTGTACCCCGGCGCGCGCTCCGCGCGC	1500
QY	1501	TGATGAGCTGTGCTCTGGGCGGAGGCGGTCTGTGACCGGCTCTGTCTGTCTTGTCTCGTGGTGG	1560
Db	1501	TGATGAGCTGTGCTCTGGGCGGAGGCGGTCTGTGACCGGCTCTGTCTGTCTTGTCTCGTGGTGG	1560
QY	1561	GCGTGTGACAGAGACCCCGGCAATCTTCGTATCTCCGGGCTCTGATGTGCAACCGGCGGATTCG	1620
Db	1561	GCGTGTGACAGAGACCCCGGCAATCTTCGTATCTCCGGGCTCTGATGTGCAACCGGCGGATTCG	1620
QY	1621	CCTCCTGCGCTGTGCGCTGTGTGCGCGGCTCTGTGCTGTGCGCGGCGGCAACCGCGGTCC	1680
Db	1621	CCTCCTGCGCTGTGCGCTGTGTGCGCGGCTCTGTGCTGTGCGCGGCGGCAACCGCGGTCC	1680

QY	1681	UGCCGTGCGGGGCCCGAACAACCGCGAAGCCGCGCGCGCTGTTCAAGCCGGAAATGCGCGGCCA	1740
Dp	1681	CGCGCTCGGGGCCCGGAACCGCGGAGCCGCGCGCTGTTCAAGCCGGAAATGCGCGGCCA	1740
QY	1741	GCCCCGCGCAGCTGGGCGCGCTGGTGTCAATGCTGTGGATCACACCGCCCTACTTCTTCC	1800
Dp	1741	GCCCCGCGCAGCTGGGCGCGCTGGTGTCAATGCTGTGGATCACACCGCCCTACTTCTTCC	1800
QY	1801	TGCCCTTCTGTGCTTCAAGCATCTCTAAGGAGCTCATCGGAGCTCATCGGAGGAGCTGTGAGCAGCC	1860
Dp	1801	TGCCCTTCTGTGCTTCAAGCATCTCTAAGGAGCTCATCGGAGGAGCTGTGAGCAGCC	1860
QY	1861	GGCGGCGCGTGCAGAGGCCCCGCGCCTCGGGGCGGAGAGAGGSCAACCGCAGACGCTCC	1920
Dp	1861	GGCGGCGCGTGCAGAGGCCCCGCGCCTCGGGGCGGAGAGAGGSCAACCGCAGACGCTCC	1920
QY	1921	GCGTCTCGCGTAAGTGAAGCCGCGGTGATTCAAAGACGCGCTGTCAAGTCGCGCCGCG	1980
Dp	1921	GCGTCTCGCGTAAGTGAAGCCGCGGTGATTCAAAGACGCGCTGTCAAGTCGCGCCGCG	1980
QY	1981	CGGGGACCGCGCAACCGTGGGTCCCTTCCCTTCTCGGCCCACTCTGGGCGCGCTTC	2040
Dp	1981	CGGGGACCGCGCAACCGTGGGTCCCTTCCCTTCTCGGCCCACTCTGGGCGCGCTTC	2040
QY	2041	CAGCTCCCTCCTAATTTGATTCAGATTCAGACCTCCACCCGCGGTACTTCCATCCCCCGAGAA	2100
Dp	2041	CAGCTCCCTCCTAATTTGATTCAGATTCAGACCTCCACCCGCGGTACTTCCATCCCCCGAGAA	2100
QY	2101	ACCATGTTCGTATCCCCCAGAGAGCTCTGGGGGACCCCGAGGCGCTTTAGAGGTGGGATCCC	2160
Dp	2101	ACCATGTTCGTATCCCCCAGAGAGCTCTGGGGGACCCCGAGGCGCTTTAGAGGTGGGATCCC	2160
QY	2161	CGGATCCGATTCAGTTAACACAGCAGTGTCTTCCAGACGCTCTGAGACAGAAAGGAGAGT	2220
Dp	2161	CGGATCCGATTCAGTTAACACAGCAGTGTCTTCCAGACGCTCTGAGACAGAAAGGAGAGT	2220
QY	2221	TGGTAATTTCTTAATCCAAACCACTGTTTGAATGCACAAAATGAGAGTCTCACAGTCTC	2280
Dp	2221	TGGTAATTTCTTAATCCAAACCACTGTTTGAATGCACAAAATGAGAGTCTCACAGTCTC	2280
QY	2281	TTGGAAGAACGAGGAGATTTCAATTAAGCTTAAATTTTATTAATGTAAGAGATCT	2340
Dp	2281	TTGGAAGAACGAGGAGATTTCAATTAAGCTTAAATTTTATTAATGTAAGAGATCT	2340
QY	2341	GAAAGCTAAGTAACCTTGTCTGTATCAAAAAGTAAGATTTGACAGACTGTGTAGA	2400
Dp	2341	GAAAGCTAAGTAACCTTGTCTGTATCAAAAAGTAAGATTTGACAGACTGTGTAGA	2400
QY	2401	ATTCTTTTCAACAGAGAACAAAACTGTCTCGAAGTGGGTTTGGAAGGAGGCTG	2460
Dp	2401	ATTCTTTTCAACAGAGAACAAAACTGTCTCGAAGTGGGTTTGGAAGGAGGCTG	2460
QY	2461	CCAAAGCGCGTGTTCAGAGAAATTCCTCTTGTTATGTCAAGCTTGATTAACA	2520
Dp	2461	CCAAAGCGCGTGTTCAGAGAAATTCCTCTTGTTATGTCAAGCTTGATTAACA	2520
QY	2521	TATGGAGACCTCAATATGCAATTTTAAACAAGTATCCATGAGCGTGAAGCTGTGAT	2580
Dp	2521	TATGGAGACCTCAATATGCAATTTTAAACAAGTATCCATGAGCGTGAAGCTGTGAT	2580
QY	2581	TTTTCTGGGGAGAGATCTGCCATGGTATGAAGATTTTCTAATTTATTTTCTGTACT	2640
Dp	2581	TTTTCTGGGGAGAGATCTGCCATGGTATGAAGATTTTCTAATTTATTTTCTGTACT	2640
QY	2641	GTTATATGCAATGTTCCTTGTGCGGGGTGGGGGTTATTTGCTTCCATAGCTTTGT	2700
Dp	2641	GTTATATGCAATGTTCCTTGTGCGGGGTGGGGGTTATTTGCTTCCATAGCTTTGT	2700
QY	2701	AATCCCGGTGCTGTCTTATATGTTCAGTGTGGTGTCTGCGCATTTATTAATTTGCTG	2760
Dp	2701	AATCCCGGTGCTGTCTTATATGTTCAGTGTGGTGTCTGCGCATTTATTAATTTGCTG	2760
QY	2761	TTGCGCTTCAACGTTGGCAGAAATCAATTTACATAAACGAAAGATTCGCGGATGATGAC	2820

Db	2761	TTGECCTTCCACGTTGGCAGAAATCATTTACATAAACCGAAGATTGCGCATCATCTAC	2820
Qy	2821	TTCTCTCAGTACTTTAACATGTCGCTCGCACTTTTCTATCTGAGCGCATCTAAC	2880
Db	2821	TTCTCTCAGTACTTTAACATGTCGCTCGCACTTTTCTATCTGAGCGCATCTAAC	2880
Qy	2881	CCATTCCTTTACACCTTCATTTCAAAAGATCAGAGCGCGGCTTTAACTGCTCTC	2940
Db	2881	CCATTCCTTTACACCTTCATTTCAAAAGATCAGAGCGCGGCTTTAACTGCTCTC	2940
Qy	2941	GCAAGGAAAGTCCAGCGCCAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGTTGCA	3000
Db	2941	GCAAGGAAAGTCCAGCGCCAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGTTGCA	3000
Qy	3001	GGGAGCACTGGAGGAGACACGGTGGCTTACCCGAGCAAAAGCGTTAACTGTAAACGATG	3060
Db	3001	GGGAGCACTGGAGGAGACACGGTGGCTTACCCGAGCAAAAGCGTTAACTGTAAACGATG	3060
Qy	3061	GGATTA 3066	
Db	3061	GGATTA 3066	

RESULT 2	ABZ79565_0	WP Sequence split into 5 fragments	LOCUS ABZ79565	Accession	ABZ79565
WP	ABZ79565_0	Fragment Name	Begin	End	
WP	ABZ79565_1		1	110000	
WP	ABZ79565_2		100001	210000	
WP	ABZ79565_3		200001	310000	
WP	ABZ79565_4		300001	410000	
ID	ABZ79565 standard; DNA; 410846 BP.		400001	410846	
AC	ABZ79565;				
XX					
XX	01-JUN-2003	(first entry)			
DE	CLLD8 and NY-REN-34 encoding DNA.				
XX					
XX	Cytostatic; gene therapy; B-cell chronic lymphocytic leukaemia; BCLL.				
KW	CLLD8; NY-REN-34; gene; ds.				
XX					
OS	Unidentified.				
FX					
FH	Key	Location/Qualifiers			
FT	CDS	294727..309803			
FT		/*tag= a			
FT		/product= "CLLD8"			
FT	CDS	313649..346509			
FT		/*tag= b			
FT		/product= "NY-REN-34"			
XX					
XX	WO2003000296-A2.				
XX					
PD	03-JAN-2003.				
XX					
XX	21-JUN-2002; 2002WO-GB002857.				
PF					
XX	21-JUN-2001; 2001GB-00015211.				
PR					
XX	(ISIS-) ISIS INNOVATIONS LTD.				
PA					
XX	Zhang Y, Moffatt M, Cookson W;				
PI					
XX					
XX	WPI; 2003-221370/21.				
DR					
XX					
PT	Treating B-cell chronic lymphocytic leukemia in an individual by				
PT	modulating the expression of the CLLD8 and/or the NY-REN-34 gene.				
PS	Disclosure; Fig 1; 154pp; English.				

Disclosure; Fig 1; 154pp; English.

CC The invention relates to a method for treating B-cell chronic lymphocytic  
CC leukemia (BCLL), comprising modulating the expression of the CLLD8  
CC and/or the NY-REN-34 gene. The polynucleotide sequence of gene product of  
CC the CLLD8 and/or NY-REN-34 gene or agent is useful for the manufacture of  
CC a diagnosis and treatment of BCLL. The current sequence represents CLLD8  
CC and NY-REN-34 encoding DNA  
XX

Sequence 410846 BP; 125177 A; 83172 C; 81704 G; 120793 T; 0 U; 0 Other;

Query Match 99.5%; Score 3050.8; DB 7; Length 110000;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3064; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

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QY 1 TTGAATTTATCTGGTCACTGCGCGCGGCTGAGCTACGCGCTGTAACTCCAGACTTTG 60
Db 3698 TTGAATTTATCTGGTCACTGCGCGCGGCTGAGCTACGCGCTGTAACTCCAGACTTTG 37047
QY 61 GAGTGAAGGCGGCTGAGCACTCGGCGGTGAGAGTTGAGACCAAGCTGGCCAACTGG 120
Db 37048 GAGTGAAGGCGGCTGAGCACTCGGCGGTGAGAGTTGAGACCAAGCTGGCCAACTGG 37107
QY 121 CGAAACCTGACTACACAAAACACAAAATTAGCCGGGCTTGGGCGCTCTGTGCTC 180
Db 37108 CGAAACCTGACTACACAAAACACAAAATTAGCCGGGCTTGGGCGCTCTGTGCTC 37167
QY 181 CCGACTCTCAGAGGCTGAGGTGAGAGACTGCTTGAAGCTTGGAGGTGAGGCTGAG 240
Db 37168 CCGACTCTCAGAGGCTGAGGTGAGAGACTGCTTGAAGCTTGGAGGTGAGGCTGAG 37227
QY 241 TGAAGTGTATGCGCGCACTTAACCTCAGCGCTGAGCGAGAGTGAAGCCCTGTCCAGA 300
Db 37228 TGAAGTGTATGCGCGCACTTAACCTCAGCGCTGAGCGAGAGTGAAGCCCTGTCCAGA 37287
QY 301 AGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAATTATTTGGTCAATTATAT 360
Db 37288 AGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAATTATTTGGTCAATTATAT 37347
QY 361 GGCAGCTCCCTCCACCACTCCGAGATTACAGAGAGAGAACTGGGCTGGCGAGAGCC 420
Db 37348 GGCAGCTCCCTCCACCACTCCGAGATTACAGAGAGAGAACTGGGCTGGCGAGAGCC 37407
QY 421 AGGACTAGCCAGATTACAGAGATTACTGGTTGAGAGCCAGATTAGACAGAGAGG 480
Db 37408 AGGACTAGCCAGATTACAGAGATTACTGGTTGAGAGCCAGATTAGAGAGAGG 37467
QY 481 CTCTAATTCTGGTCTAGACTGCCCTCTATTATTATTAGATTATGGCTTCTGAGAGATTA 540
Db 37468 CTCTAATTCTGGTCTAGACTGCCCTCTATTATTATTAGATTATGGCTTCTGAGAGATTA 37527
QY 541 CCATGAGCCCTCTCCACCGTCAAGCGGAGCTACCAAGCCACAGCCAGATCCCTTGA 600
Db 37528 CCATGAGCCCTCTCCACCGTCAAGCGGAGCTACCAAGCCACAGATCCCTTGA 37587
QY 601 AGGTGCCCGAGATCAAGACTGACAAAGCGCCCGTACAGTGTCTGTAACTGAA 660
Db 37588 AGGTGCCCGAGATCAAGACTGACAAAGCGCCCGTACAGTGTCTGTAACTGAA 37647
QY 661 GCGTCTAGGATGACAGATCGCTCAAGCGGAGTGGGCTGGTGGCTTAAAGGCGCC 720
Db 37648 GCGTCTAGGATGACAGATCGCTCAAGCGGAGTGGGCTGGTGGCTTAAAGGCGCC 37707
QY 721 GGGTATTCCAGTTAGTGAAGAGAAAGCGCCCTGAGACTGATGAGCCCGGAGAGGCG 780
Db 37708 GGGTATTCCAGTTAGTGAAGAGAAAGCGCCCTGAGACTGATGAGCCCGGAGAGGCG 37767
QY 781 CGGAGCGGAGAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGACTGCGCGAG 840
Db 37768 CGGAGCGGAGAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGACTGCGCGAG 37827
QY 841 CTAGCTCGGAGAGCGCTCGAGCCCAAGCCCGAGAGCGCTTCTGCGCCCGGAGAGCGCA 900
Db 37828 CTAGCTCGGAGAGCGCTCGAGCCCAAGCCCGAGAGCGCTTCTGCGCCCGGAGAGCGCA 37887
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QY 901 GCGAGCGCTCCGCGCTGTGACCTGCGCGCGCCGACAGCTGGCGGCTGGAAAAAGAGCG 960
Db 37888 GCGAGCGCTCCGCGCTGTGACCTGCGCGCGCCGACAGCTGGCGGCTGGAAAAAGAGCG 37947
QY 961 CTCAACGAGAGGAGCAAGCGCCAGAGCTCCAGCCGACCCGAGACCGCGCGCGCGCG 1020
Db 37948 CTCAACGAGAGGAGCAAGCGCCAGAGCTCCAGCCGACCCGAGAGCGCGCGCGCGCG 38007
QY 1021 GAGCAACCATAGGAGAGCGCCCTTGAAACGGACAGCGCCCGGAGAGGAGGAGGAGCGCG 1080
Db 38008 GAGCAACCATAGGAGAGCGCCCTTGAAACGGACAGCGCCCGGAGAGGAGGAGGAGCGCG 38067
QY 1081 CGTGGCCCGCGCTGCCCTTGGACAGAGAGCGCGCTGCGCCCTTCCCTGGGAGCG 1140
Db 38068 CGTGGCCCGCGCTGCCCTTGGAGAGAGCGCGCTGCGCCCTTCCCTGGGAGCGCG 38127
QY 1141 TGTGCGCGTGAAGCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 38128 TGTGCGCGTGAAGCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 38187
QY 1201 TGACGATGATGCTATCGGCGGCTACCGGAGCATGAGGAGCAACCACTTGTACTGCG 1260
Db 38188 TGACGATGATGCTATCGGCGGCTACCGGAGCATGAGGAGCAACCACTTGTACTGCG 38247
QY 1261 GCAGCATGGCGGTGTCCAGCTTACTATCTGTGCGGCTGCGGTTGACCTGACCGCC 1320
Db 38248 GCAGCATGGCGGTGTCCAGCTTACTATCTGTGCGGCTGCGGTTGACCTGACCGCC 38307
QY 1321 TCTGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
Db 38308 TCTGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 38367
QY 1381 GCGAGGCGCTGACCTACCGACCGCTGTGACATGACCGCGCTCAGCGTGAAGCGCTACC 1440
Db 38368 GCGAGGCGCTGACCTACCGACCGCTGTGACATGACCGCGCTCAGCGTGAAGCGCTACC 38427
QY 1441 TGGCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
Db 38428 TGGCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 38487
QY 1501 TCAATGCTGTGCTTGGGCGCGTGTGCTGTCTCTGCGGCTCCTTGTGCTGCTGCTG 1560
Db 38488 TCAATGCTGTGCTTGGGCGCGTGTGCTGTCTCTGCGGCTCCTTGTGCTGCTGCTG 38547
QY 1561 GCGTCAAGAGAGACCGCGGATCTCGTGTAGTCCCGGCGCTCAATGAGACCGCGGATG 1620
Db 38548 GCGTCAAGAGAGACCGCGGATCTCGTGTAGTCCCGGCGCTCAATGAGACCGCGGATG 38607
QY 1621 CTTGCTGCTCTGCGCTGCTGCGCGCGCTCTGAGCTCTGAGCGGAGCGCCGCTGCC 1680
Db 38608 CTTGCTGCTCTGCGCTGCTGCGCGCGCTCTGAGCTCTGAGCGGAGCGCCGCTGCC 38667
QY 1681 GCGCTGCGGCGCGAGACCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1740
Db 38668 GCGCTGCGGCGCGAGACCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 38727
QY 1741 GCGCGCGGAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1800
Db 38728 GCGCGCGGAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 38787
QY 1801 TGCCTTTCTGTGCTCAGAGATCTCTACGAGGCTCATTCGAGGAGAGCTGTGAGAGCGCC 1860
Db 38788 TGCCTTTCTGTGCTCAGAGATCTCTACGAGGCTCATTCGAGGAGAGCTGTGAGAGCGCC 38847
QY 1861 GCGGCGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAGAGAGCGCG 1920
Db 38848 GCGGCGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAGAGAGCGCG 38907
QY 1921 GCGTCTGCTGATGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1980
Db 38908 GCGTCTGCTGATGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 38967
QY 1981 CGGAGACCGGCAAGCTGAGGTCCTTCCCTGCTGCGCCAGCTCTGGGCGCGCGCTTC 2040
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Db 38968 CGGGAGACCGGCAAGCTGGGTCCCTTCCCTCTGCTCGCCAGCTCTGGGGCGCGCTTC 39027  
QY 2041 CAGCTCCC - TCCATTTCGATTCAGCTCCACCCGCGGATCTCCCATCCCCGAGA 2098  
Db 39028 CAGCTCCCTTTCCTATTTCATTCAGCCCTCCACCCGCGGATCTCCCATCCCCGAGA 39087  
QY 2099 AAACCATGTCTGTCCCGCCGAGAGCTCTGGGGGAGACCCAGCGCGCTTTGAGGGTGGGATC 2158  
Db 39088 AAACCATGTCTGTCTCCCGCCGAGAGCTCTGGGGGAGACCCAGCGCGCTTTGAGGGTGGGATC 39147  
QY 2159 CCGGATCCGATTCAGTACAGCAAGTCTTTTCAGAGCTCTGAGACCAAGAGAGA 2218  
Db 39148 CCGGATCCGATTCAGTACAGCAAGTCTTTTCAGAGCTCTGAGACCAAGAGAGA 39207  
QY 2219 GTTGGTATCTTAATCCACCACTGTTAGTCCCAATGAGAGTCTCACAGTGC 2278  
Db 39208 GTTGGTATCTTAATCCACCACTGTTAGTCCCAATGAGAGTCTCACAGTGC 39267  
QY 2279 TCTTGAGAGACGAGGAGATTCATTAGCTAAATTTTATTATTTATGTAAGTATG 2338  
Db 39268 TCTTGAGAGACGAGGAGATTCATTAGCTAAATTTTATTATTTATGTAAGTATG 39327  
QY 2339 CTGAGGCTTAAGTAACTTTGCTCTGATCAAAAAGTAAAGATTGGCAGACCTGTGTA 2398  
Db 39328 CTGAGGCTTAAGTAACTTTGCTCTGATCAAAAAGTAAAGATTGGCAGACCTGTGTA 39387  
QY 2399 GAATCTTTTCAACAGAGAACAGAAAACCTTGCTCCGAGTGGTGTGTGGAAGAACCC 2458  
Db 39388 GAATCTTTTCAACAGAGAACAGAAAACCTTGCTCCGAGTGGTGTGTGGAAGAACCC 39447  
QY 2459 TGCCAGCGCGCTTGTTCAGAGAAATTGCTCTCTGTTATGTCCAGCTTGATPACA 2518  
Db 39448 TGCCAGCGCGCTTGTTCAGAGAAATTGCTCTCTGTTATGTCCAGCTTGATPACA 39507  
QY 2519 CATATGGAGGCTACTATGCAATTTTAAAGCAAGTATCCAGAGCTGAGCCTGTGCA 2578  
Db 39508 CATATGGAGGCTACTATGCAATTTTAAAGCAAGTATCCAGAGCTGAGCCTGTGCA 39567  
QY 2579 TTTTTCCTGGGGTGAAGATCTGCTAGGTAGAGTTCCTTAATTTATTTGCTGTAC 2638  
Db 39568 TTTTTCCTGGGGTGAAGATCTGCTAGGTAGAGTTCCTTAATTTATTTGCTGTAC 39627  
QY 2639 TTGTTATTCAGAGATGCTCTGTCGCGGGTGGGGTATTTGCTCCCAATGCTTTG 2698  
Db 39628 TTGTTATTCAGAGATGCTCTGTCGCGGGTGGGGTATTTGCTCCCAATGCTTTG 39687  
QY 2699 TTAATCCCGAGTGTGCTTATATGTTGAGTGTGTGTGATCTGAGCATTTAATTTGCT 2758  
Db 39688 TTAATCCCGAGTGTGCTTATATGTTGAGTGTGTGTGATCTGAGCATTTAATTTGCT 39747  
QY 2759 GGTTCCTTCAGAGTGTGCTGTCGCGGGTGGGGTATTTGCTCCCAATGCTTTG 2818  
Db 39748 GGTTCCTTCAGAGTGTGCTGTCGCGGGTGGGGTATTTGCTCCCAATGCTTTG 39807  
QY 2819 ACTTCTCAGACTTTAATCAATCGTGTGCTGCACTTTTCTATGAGCCATCTATCA 2878  
Db 39808 ACTTCTCAGACTTTAATCAATCGTGTGCTGCACTTTTCTATGAGCCATCTATCA 39867  
QY 2879 ACCCAATCTCTACAACTGATTTTAAAGAGTACAGAGCGCGGCTTTAACTGCTGC 2938  
Db 39868 ACCCAATCTCTACAACTGATTTTAAAGAGTACAGAGCGCGGCTTTAACTGCTGC 39927  
QY 2939 TGGCAAGGAGTCCAGCGCGGAGGCTTCCAGAGAGAGGAGCACTGCGGGGGAAGTTG 2998  
Db 39928 TGGCAAGGAGTCCAGCGCGGAGGCTTCCAGAGAGAGGAGCACTGCGGGGGAAGTTG 39987  
QY 2999 CAGGGAGCACTGAGAGAGACACGCTGGGCTACACCGAGCAAGGCTTAACTGAAGAGCA 3058  
Db 39988 CAGGGAGCACTGAGAGAGACACGCTGGGCTACACCGAGCAAGGCTTAACTGAAGAGCA 40047  
QY 3059 TGGGATTA 3066  
|||||

Db 40048 TGGGATTA 40055  
RESULT 3  
ID AAA46116  
AAA46116 standard; cDNA: 2040 BP.  
XX AAA46116;  
XX 22-AUG-2000 (first entry)  
DE Human G protein coupled receptor hGPR38 (V297K) cDNA SEQ ID NO:129.  
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;  
KW Identification; agonist; screening; therapeutic; pharmaceutical; mutant;  
KW ss.  
OS Homo sapiens.  
XX Synthetic.  
XX WO200022131-A2.  
XX 20-APR-2000.  
XX PD  
XX 13-OCT-1999; 99WO-US024065.  
XX PF  
XX 13-OCT-1998; 98US-00170496.  
XX PR 12-NOV-1998; 98US-0108022P.  
XX PR 20-NOV-1998; 98US-0109213P.  
XX PR 27-NOV-1998; 98US-0110060P.  
XX PR 16-FEB-1999; 99US-0120416P.  
XX PR 26-FEB-1999; 99US-0121852P.  
XX PR 12-MAR-1999; 99US-0123944P.  
XX PR 12-MAR-1999; 99US-0123945P.  
XX PR 12-MAR-1999; 99US-0123946P.  
XX PR 12-MAR-1999; 99US-0123948P.  
XX PR 12-MAR-1999; 99US-0123949P.  
XX PR 12-MAR-1999; 99US-0123951P.  
XX PR 28-MAY-1999; 99US-0136436P.  
XX PR 28-MAY-1999; 99US-0136437P.  
XX PR 28-MAY-1999; 99US-0136439P.  
XX PR 28-MAY-1999; 99US-0137127P.  
XX PR 28-MAY-1999; 99US-0137127P.  
XX PR 28-MAY-1999; 99US-0137131P.  
XX PR 28-MAY-1999; 99US-0137567P.  
XX PR 29-JUN-1999; 99US-0141448P.  
XX PR 27-AUG-1999; 99US-0151114P.  
XX PR 03-SEP-1999; 99US-0152524P.  
XX PR 29-SEP-1999; 99US-0156555P.  
XX PR 29-SEP-1999; 99US-0156533P.  
XX PR 29-SEP-1999; 99US-0156534P.  
XX PR 29-SEP-1999; 99US-0156534P.  
XX PR 01-OCT-1999; 99US-0157280P.  
XX PR 01-OCT-1999; 99US-0157281P.  
XX PR 01-OCT-1999; 99US-0157282P.  
XX PR 01-OCT-1999; 99US-0157293P.  
XX PR 01-OCT-1999; 99US-0157294P.  
XX PR 12-OCT-1999; 99US-00416760.  
XX PR 12-OCT-1999; 99US-00417044.  
XX PA  
XX (AREN-) ARENA PHARM INC.  
XX Behan DP, Lehmann-Bruinema K, Chalmers DT, Chen R, Dang HT;  
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
XX WPI; 2000-317986/27.  
XX P-PSDB; AAB02854.  
XX Non-endogenous, human G protein-coupled receptors for screening receptor,  
XX Inverse or partial agonists useful as therapeutic agents.  
XX Example 2; Page 166-168; 187pp; English.  
XX The present invention describes transmembrane receptors, preferably human







us-09-719-485-1.rng

Query Match	33.9%	Score 1038	DB 4	Length 1161	
Best Local Similarity	99.8%	Prod. No. 3.5e-163			
Matches 1050	Conservative	0	Mismatches	0	Indels 2
					Gaps 1
QY	1029	ATGGGCAACCCCTTGAAACGACGACGAGCGCCCTCGAGGGGAGCGCGGAGCCGCTGGCC	1088		
Db	1	ATGGGCAACCCCTTGAAACGACGACGAGCGCCCTCGAGGGGAGCGCGGAGCCGCTGGCC	60		
QY	1089	GCGTGGCCGCTTGGGACGAGCGCGCGCTGGCCCTTCCCTGGGGGAGCTGATGCG	1148		
Db	61	GCGTGGCCGCTTGGGACGAGCGCGCGCTGGCCCTTCCCTGGGGGAGCTGATGCG	120		
QY	1149	GTCACCGCTGTGTGCTGTGCTCTGTTCTGTGCTCGGGGTGAGCGGCAACGTGTGACCGTG	1208		
Db	121	GTCACCGCTGTGTGCTGTGCTCTGTTCTGTGCTCGGGGTGAGCGGCAACGTGTGACCGTG	180		
QY	1209	ATGTGTAATCGGGCGCTTACCGGAGACATCGGACCAACCAACCAACTTGTATCCTGGGAGAGATG	1258		
Db	181	ATGTGTAATCGGGCGCTTACCGGAGATCGGACCAACCAACCAACTTGTATCCTGGGAGAGATG	240		
QY	1269	GCGGTATCCGACCTACTCATCTCTGCTGGGCTGGCGCTGCTTCGACTGTACCCGCTCTGGCGC	1328		
Db	241	GCGGTATCCGACCTACTCATCTCTGCTGGGCTGGCGCTGCTTCGACTGTACCCGCTCTGGCGC	300		
QY	1329	TGCGGACCTGTGGTGTGTGCGGAGCGCTGCTCTGCGCTGTGCTCTTACGTGTGGAGAGGC	1388		
Db	301	TGCGGACCTGTGGTGTGTGCGGAGCGCTGCTCTGCGCTGTGCTCTTACGTGTGGAGAGGC	360		
QY	1389	TGCACCTTACGCAACGCTGTGCTGTGACATAGACGCGCTACGCGTACCGGCTACTGAGCATC	1448		
Db	361	TGCACCTTACGCAACGCTGTGCTGTGACATAGACGCGCTACGCGTACCGGCTACTGAGCATC	420		
QY	1449	TGCCGACCGCTTCGCGGCGCGCGGTGTTGTACACCGGAGCGCGGTTCGCGCGCTCATCGCT	1508		
Db	421	TGCCGACCGCTTCGCGGCGCGCGGTGTTGTGTACACCGGAGCGCGGTTCGCGCGCTCATCGCT	480		
QY	1509	GTGCTCTGGGCGCGTGGGCGCTCTCTGCGCGGATCCCTTGTGTCGTGTGGGGGTGAG	1568		
Db	481	GTGCTCTGGGCGCGTGGGCGCTCTCTGCGCGGATCCCTTGTGTCGTGTGGGGGTGAG	540		
QY	1569	CAGAACCCCGGCATCTCCGTAGTCCCGGCGCTCATGACACCGCGCGATCGCTCTCG	1628		
Db	541	CAGAACCCCGGCATCTCCGTAGTCCCGGCGCTCATGATGACACCGCGCGATCGCTCTCG	600		
QY	1629	CTCTCGCCTGTGTGCGCGCTCTTGTGCTCTGCGGGGCGCACCGCGTCCCCGCTGTG	1688		
Db	601	CTCTCGCCTGTGTGCGCGCTCTTGTGCTCTGCGGGGCGCACCGCGTCCCCGCTGTG	660		
QY	1689	GGGCGCGAGACCGGAGAGGCGCGCGCGCTGTTCAGCGCGCATATCGGCGCAGGCGCGCG	1748		
Db	661	GGGCGCGAGACCGGAGAGGCGCGCGCGCTGTTCAGCGCGCATATCGGCGCGAGGCGCGCG	720		
QY	1749	CAGCTGGAGCGGTGGGTGTATGTGTGGGTACACACCGCTTACTTCTCTGCTCTT	1808		
Db	721	CAGCTGGAGCGGTGGGTGTATGTGTGGGTACACACCGCTTACTTCTCTGCTCTT	780		
QY	1809	CTGTGGCTCAGCATCTCTACGGGCTATCGGGGCGGAGCGTGTGAGGAGCGCGCGCG	1868		
Db	781	CTGTGGCTCAGCATCTCTACGGGCTATCGGGGCGGAGCGTGTGAGGAGCGCGCGCGCG	840		
QY	1869	CTGGGAGCGCGCGCGCTTCGGGCGGAGAGAGACCAACCGGACGACCTGTGCGGTCTG	1928		
Db	841	CTGGGAGCGCGCGCGCTTCGGGCGGAGAGAGACCAACCGGACGACCTGTGCGGTCTG	900		
QY	1929	CGTAAATGTGAGACCGCGCTGTTCCAAAGACCGCTGTGAGATCGCGCGCGCGGAGAC	1988		
Db	901	CGTAAATGTGAGACCGCGCTGTTCCAAAGACCGCTGTGAGATCGCGCGCGCGGAGAC	960		
QY	1989	GCGCAAAACGCTGGGTGCCCTTCCCTCTGCGCAGGCTGTGTGGGCGCGCTTCCAGGCTCC	2048		
Db	961	GCGCAAAACGCTGGGTGCCCTTCCCTCTGCGCAGGCTGTGTGGGCGCGCTTCCAGGCTCC	1022		







XX (ZYMO ) ZYMOGENETICS INC.  
XA  
XP  
XI Sheppard PO, Jaspers SR, Deisher TA, Bishop JD;  
PI WPI; 2001-355879/37.  
DR P-PsDB; AAB62652.  
XX  
XX  
PT Forming reversible peptide receptor complex for purifying cell and  
PS peptides, stimulating signal transduction and modulating hormone  
PS secretion, involves contacting a receptor with zsig33 polypeptide.  
PS Disclosure; Page 102-104; 11pp; English.

The invention relates to a method of forming a reversible peptide-receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (comprising residues 24-37 of AAB62649), where the receptor binds to the zsig33 peptide. The method is useful for purifying cells, purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, gastric contractility, nutrient uptake, secretion of digestive and pancreatic enzymes and hormones, secretion of insulin-like growth factor I, secretion of non-zsig33 proteins. It is useful for modulating growth hormone secretion in a mammal having a disease associated with abnormal levels of growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, skeletal dysplasia, immune suppression, obesity, growth retardation, protein catabolic responses after surgery, cachexia, protein loss, dwarfism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety regulation, glucose absorption and metabolism and neuropathy-associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the DNA encoding the long form of molfin receptor, GPR-38A (one of the two isoforms of GPR38 which result from alternative splicing). GPR38 has homology to the human G-protein coupled receptor, GHS-R

SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match 29.4%; Score 901; DB 4; Length 1239;  
Best Local Similarity 100.0%; Pred. No. 1.9e-140;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1029 ATGGGCAACCCCTTGAAAGCGACGAGCGCCCCGAGGAGCGCCGTGGGCC 1088  
Db 1 ATGGGCAACCCCTTGAAAGCGACGAGCGCCCCGAGGAGCGCCGTGGGCC 60

QY 1089 GCGCGCGCGCCTTGGAGCGAGCGCGCGTCGCCTTCCCCTGGGGGCGCTGGTGGCG 1148  
Db 61 GCGCGCGCGCCTTGGAGCGAGCGCGCGTCGCCTTCCCCTGGGGGCGCTGGTGGCG 120

QY 1149 GTGACCGCTGTGTGCTGTGCTGTTCGTGCTGGGAGTAGCGCATGATACCCTG 1208  
Db 121 GTGACCGCTGTGTGCTGTGCTGTTCGTGCTGGGAGTAGCGCATGATACCCTG 180

QY 1209 ATGCGTAGCGGAGCGTAACGGGGAATMGGGACAACACACACTTTGACTGGGAGATG 1268  
Db 181 ATGCGTAGCGGAGCGTAACGGGGAATMGGGACAACACACACTTTGACTGGGAGATG 240

QY 1269 GCCGTGTCCAGCTACTCATCTGCTGGGCTGGCGATTGACCTGTACCGGCTCTGGGCG 1328  
Db 241 GCCGTGTCCAGCTACTCATCTGCTGGGCTGGCGATTGACCTGTACCGGCTCTGGGCG 300

QY 1329 TCGGGCGCCCTGGGGGTTCGGGGCGCTGTCTGCGCGCTGTCCCTTACATGTGGGCGAGGGCG 1388  
Db 301 TCGGGCGCCCTGGGGGTTCGGGGCGCTGTCTGCGCGCTGTCCCTTACATGTGGGCGAGGGCG 360

QY 1389 TGCACTTACGCAAGCGTGTGTCGATACGATACCGCGCTCACAGCGGTACCTGGCCATC 1448  
Db 361 TGCACTTACGCAAGCGTGTGTCGATACGATACCGCGCTCACAGCGGTACCTGGCCATC 420

QY 1449 TGCAGCCCGCTCCGCGCCCGCTGTTGGTATACCCGAGCGCGCGTGTCCGCGCGCTATCGCT 1508

Dd		421.	TCCGCGCCGCTCCGGGCCCGGATTTGGTCAACCGAGCGCGGTCCGCTATGCT	480
Oy		1509	GTCCTCTGAGCCGTGGCCGCTGCTCTCTGC CGGTCCTTCTTGTTCTTGAGGAGTGCAG	1568
Dd		481	GTGCTCTGAGCCGAGGCGCTGCTCTCTGCGCGGTCCCTTTGTTCTTGAGGAGTGCAG	540
Oy		1569	CAGGACCCCCGAGATCTCCTTAGTCTCCGAGGCTCATATGGCACCGCGGAAATGCTCTTCG	1628
Dd		541	CAGGACCCCCGAGATCTCCTTAGTCTCCGAGGCTCATATGGCACCGCGGAAATGCTCTTCG	600
Oy		1629	CCTCTCGCCTGTGCGCGCTCTCTGAGCTTCGCGGAGCGCACCGCGTCCCGCGGTG	1688
Dd		601	CCTCTCGCCTGTGCGCGCTCTCTGAGCTTCGCGGAGCGCACCGCGTCCCGCGGTG	660
Oy		1689	GAGCCCGAGACCGCGGAGGCGCGCGCTGTTACCGCGAATGCGGCGGAGCCCGCG	1748
Dd		661	GAGCCCGAGACCGCGGAGGCGCGCGCTGTTACCGCGAATGCGGCGGAGCCCGCG	720
Oy		1749	CAGCTGGGCGCGCTGCGGTCATGCTTGAGGTACAACGCGCTACTTCTTCGCGCTTT	1808
Dd		721	CAGCTGGGCGCGCTGCGGTCATGCTTGAGGTACAACGCGCTACTTCTTCGCGCTTT	780
Oy		1809	CTGTGCTCTAGCATCTCTTAACGAGCTATCGGAGCGGAGCTGTGAGACACCGCGAGCG	1868
Dd		781	CTGTGCTCTAGCATCTCTTAACGAGCTATCGGAGCGGAGCTGTGAGACACCGCGAGCG	840
Oy		1869	CTGGGAGGCGCGCGCGCTCTGGGCGCGGAGAGGACACCGGCTAGATCGTCCGCTCTG	1928
Dd		841	CTGGGAGGCGCGCGCGCTCTGGGCGCGGAGAGGACACCGGCTAGATCGTCCGCTCTG	900
Oy		1929	C 1929	
Dd		901	C 901	
<b>RESULT 10</b>				
ABK90132	ID	ABK90132	standard; DNA; 1239 BP.	
XX AC	AC	ABK90132;		
XX XX	DT	21-OCT-2002	(first entry)	
DE DX	DNA encoding human G protein-coupled receptor 38 (GPR38).			
KW KW	Human; G protein-coupled receptor 38; receptor; GPR38; gene; ds;			
KM KM	Alzheimer's disease; Parkinson's disease; ulcerative colitis;			
KX KX	Crohn's disease; Hodgkin's disease; glioblastoma; breast carcinoma;			
KY KY	colon carcinoma; lung small cell carcinoma; lung adenocarcinoma;			
XX XX	pancreatic small cell carcinoma; pancreatic adenocarcinoma.			
OS OS	Homo sapiens.			
XX Key	Location/Qualifiers			
FT FT	1..1239			
FT FT	/*tag= a			
XX FT	/product= "human G protein-coupled receptor 38 (GPR38)"			
PN PN	MO200257791-A2.			
XX PD	25-JUL-2002.			
XX PF	29-NOV-2001; 2001WO-US045219.			
XX PR	29-NOV-2000; 2000US-0250251P.			
XX PR	30-NOV-2000; 2000US-0250452P.			
PA PA	(LIFE-) LIFESPAN BIOSCIENCES INC.			
XI XI	Brown JP, Burner GC, Roush CL, Kulander BG;			
XX XR	MPI; 2002-566812/50.			



DR P-PSDB; ABG30936

PT Assay for detecting Alzheimer's disease, Parkinson's disease, ulcerative  
PT colitis, Crohn's disease, Hodgkin's disease, glioblastoma or carcinoma,  
PT comprises using a binding partner for G protein coupled receptor 38.

PS Disclosure; Fig 1; 112pp; English.

CC The present invention relates to a new assay method that involves  
CC contacting a binding partner specific for G protein coupled receptor  
CC (GPR) 38 with specific cells. The method of the invention is useful for  
CC the detection of an increased risk of Alzheimer's disease, Parkinson's  
CC disease, ulcerative colitis, Crohn's disease, Hodgkin's disease,  
CC glioblastoma, or carcinoma. GPR 38 is used to manufacture a medicament  
CC for inhibiting, treating or preventing Alzheimer's disease, Parkinson's  
CC disease, ulcerative colitis, Crohn's disease, Hodgkin's disease,  
CC glioblastoma, breast carcinoma, colon carcinoma, lung small cell  
CC carcinoma, lung adenocarcinoma, pancreatic small cell carcinoma, and  
CC pancreatic adenocarcinoma. An agonist or antagonist to GPR 38 are used to  
CC manufacture a medicament able to reduce the symptoms of these diseases.  
CC Nucleic acids encoding GPR 38 can also be used to treat the diseases. The  
CC present nucleic acid sequence encodes the human G protein- coupled  
CC receptor 38 (GPR38) of the invention

Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match	Score	DB	Length
29.4%	901	6	1239

Matches	901;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
---------	------	--------------	----	------------	----	--------	----	------	---

1029 ATGGGCAGCCCTGTGAACGGCAGCAGGCCCGGAGCGCCCTGGCC 108

QY	1029	TTGGGACACCCCTGGAAAGGAGAGCAAGCCGCCGAGGGGGAGCGGGAGCCCGCTGGCGC	108
Db	1	ATGGGACACCCCTGGAAAGGAGAGCAAGCCGCCGAGGGGGAGCGGGAGCCCGCTGGCGC	60
QY	1089	GCGCTGCCGCTTGGAGAGAGAGCGCGCTGCTGCGCCCTTTCCTCGGGGGCGCTGGTGGC	1148
Db	61	GCGCTGCCGCTTGGAGAGAGAGCGCGCTGCTGCGCCCTTTCCTCGGGGGCGCTGGTGGC	120
QY	1149	GTGACCGCTGTGTGCTGTGACTGTTCCTGTGTGGGGGTGAGCGGCAAGTGTGACCGTG	1208
Db	121	GTGACCGCTGTGTGCTGTGACTGTTCCTGTGTGGGGGTGAGCGGCAAGTGTGACCGTG	180
QY	1209	ATGCTGATCGGGCGGTACCGGGACATGGGGAACACACCAACTTGTACCTGGGACAGATG	1268
Db	181	ATGCTGATCGGGCGGTACCGGGACATGGGGAACACACCAACTTGTACCTGGGACAGATG	240
QY	1269	GCCGTGTCGGACTTACTATCTCTGCTCGGGGTCGGCCGTTCGACTGTATACCGCCTTGCGGC	1328
Db	241	GCCGTGTCGGACTTACTATCTCTGCTCGGGGTCGGCCGTTCGACTGTATACCGCCTTGCGGC	300
QY	1329	TGCGGGCCCTGGGTGTGGGGCGCGGTGCTTCGCGCGCTGCTCCCTTACGTGGGGAGAGGC	1388
Db	301	TGCGGGCCCTGGGTGTGGGGCGCGGTGCTTCGCGCGCTGCTCCCTTACGTGGGGAGAGGC	360
QY	1389	TGCACCTTACGCCACGCTGTGTACATGACACCGCGCTCAAGCTGTGAGCGCTTACTGTGCATC	1448
Db	361	TGCACCTTACGCCACGCTGTGTACATGACACCGCGCTCAAGCTGTGAGCGCTTACTGTGCATC	420
QY	1449	TGCGGCGCCGCTCGGGGCGCGGCGTCTTGGTCAACCGGAGCGCGGTGCGGCGCTCATGCT	1508
Db	421	TGCGGCGCCGCTCGGGGCGCGGCGTCTTGGTCAACCGGAGCGCGGTGCGGCGCTCATGCT	480
QY	1509	GTGCTGTGGGCGGTGGCGGCTGTCTCTCTGTGCGGTCCTTCTTGTCTGTGTGGGGCTCGAG	1568
Db	481	GTGCTGTGGGCGGTGGCGGCTGTCTCTCTGTGCGGTCCTTCTTGTCTGTGTGGGGCTCGAG	540
QY	1569	CAGGACCCCGGAGATTCACGTAGTCCCGGGGCTCAATGAGACCGGCGGATCGCCTCTCG	1628
Db	541	CAGGACCCCGGAGATTCACGTAGTCCCGGGGCTCAATGAGACCGGCGGATCGCCTCTCG	600
QY	1629	CCTCTGCGCTCGTGGCTGCTCTTGTGGCTCTGTGGGAGCGCAAGCGTCTCCCGCGCTCG	1688
Db	601	CCTCTGCGCTCGTGGCTCTTGTGGCTCTGTGGGAGCGCAAGCGCGTCTCCCGCGCTCG	660

## RESULT 11

ID	ABZ42842	standard; DNA; 1239 BP
vv		

AC ABZ42842

DT 04-MAR-2003 (first entry)  
 YY

DE Human motilin receptor GPR38 nucleotide SEQ ID NO:4/2

KM G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KM G protein-coupled receptor modulator; antibody; immune-related disease;  
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KM immunological-related cell proliferative disease; autoimmune disease;  
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy  
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KM postnatal anxiety; depression; schizophrenia; dementia; memory loss;  
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KM ulcer; gene; ds.

OS Homo sapiens.

PN WO200261087-A2

PD 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US050107

PR 19-DEC-2000; 2000US-0257144P.  
XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX

PI Burmer GC, Roush CL, Brown JP, XY

DR WP1: 2003-046/18/04  
DR P-PSDB: ABP61993

XX	New isolated anti:
PT	

PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or

PS Disclosure; Fig 1; 523pp; English.

245 The present invention describes antigenic peptides (1) comprising: (a)  
246 any one of 1601 sequences (see ABP2019 to ABP3619) of 12-24 amino  
247 acids. Also described: (1) an assay for the detection of a particular G  
248 protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
249 and (2) an isolated antibody having high specificity and high affinity or



status of many C residues to be determined simultaneously. AB013410-AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention

Sequence 1179 BP; 178 A; 159 C; 443 G; 399 T; 0 U; 0 Other;

Query Match 24.8%; Score 761.4; DB 6; Length 1179;  
Best Local Similarity 77.9%; Pred. No. 2,7e-117;  
Matches 918; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

588 CAGATCCCTTGAAGGTGCGCGGAGTACCAAGTACGACAAAGCGCCGTACAGTGCAG 647  
Db CAATTCCTTGAAGGTGCGCGGAGTACCAAGTACGACAAAGCGCCGTACAGTGCAG 1120  
QY TCCTGTAAACCAAGCTGTAGGGTGAAGACATGCTCACCAGACCGGGTAAAGGCTCTG 707  
Db TCCTGTAAACCAAGCTGTAGGGTGAAGACATGCTCACCAGACCGGGTAAAGGCTCTG 1060  
QY CGCTAAAGGCGCGCGGTATTCAGTGTAGAGGAGGAGCGCCCTGGAATCGATGGCG 767  
Db CGCTAAAGGCGCGCGGTATTCAGTGTAGAGGAGGAGCGCCCTGGAATCGATGGCG 1000  
QY CGCTAAAGGCGCGCGGTATTCAGTGTAGAGGAGGAGCGCCCTGGAATCGATGGCG 1000  
Db CGCTAAAGGCGCGCGGTATTCAGTGTAGAGGAGGAGCGCCCTGGAATCGATGGCG 940  
QY CCGGAGAGGCGCGCGGAGCGAGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 827  
Db CCGGAGAGGCGCGCGGAGCGAGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 940  
QY AGACTGCGCGAGTACTGCTGGAGAGCGCTGTGAGAGCCGACCCCGCAAGCCGCTTCG 887  
Db AACTGACGCGAGTACTGCTGGAGAGCGCTGTGAGAGCCGACCCCGCAAGCCGCTTCG 880  
QY GCGCGGAGCGCGAGCGCGCTCGCGCGCTGACCTGCGCGCGCGCGCGCGCGCGCGCG 947  
Db GCGCGGAGCGCGAGCGCGCTCGCGCGCTGACCTGCGCGCGCGCGCGCGCGCGCGCG 820  
QY GCGGAGAGGCGCGCTCACCAGAGGAGCACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1007  
Db AAAAAAAGCGCTCACCAGAGGAGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 760  
QY CCGGCGCGCGCGCGAGCGACCGATGGGAGCGCCCTGGAAGCGCGCGCGCGCGCGCG 1067  
Db CGACACCGCGCGAGGAGCGACCGATGGGAGCGCCCTGGAAGCGCGCGCGCGCGCGCG 700  
QY GCGGAGAGCGCGCGCTGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 1127  
Db AGCGGAGAGCGCGCGCTGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 640  
QY CCGCTGGGGGGCGCTGCTGCGCGTACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1187  
Db CCGCTGGGGGGCGCTGCTGCGCGTACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 580  
QY CCGCTGGGGGGCGCTGCTGCGCGTACCGCGTATATACCGTATATATGCTGCTGGAATA 520  
Db AGCGGAGAGCGCGCGTATGCTGATGCGCGCGTACCGCGGACATGCGGAGCACACACC 1247  
QY AAGCGAGAGCGCGTATGCTGATGCGCGCGTACCGCGGACATGCGGAGCACACACC 520  
Db AACTGTACTGCGGAGCGCGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1307  
QY AACTGTACTGCGGAGCGCGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 460  
Db GACCTGTACCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1367  
QY GACCTGTACCGCGCTGCTG 400  
Db GACCTGTACCGCGCTGCTG 1427  
QY TCCTGTACTGCGGAGCGCGCTGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1427  
Db TCCTGTACTGCGGAGCGCGCTGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 340  
QY GTCGAGCGCGTACCTGCG 1487  
Db GTCGAGCGCGTACCTGCG 280  
QY CGCGTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1547

Db 279 CGCGTCCGCGCGCTCATGCTATTAACCGTAAACCGTAACTCTCTACCGATCCCTC 220  
QY 1548 TTGTTCTGTGTGGGCGTGAAGAGACCCCGCATCTTCGTATGTCGGGCGCTCAATGCG 1607  
Db TTATTCCTTAATTAAGTGAACAAACCCCGCATCTCGTATCCCAACCTCAATTAAC 160  
QY 1608 ACCGCGCGGATGCGCTCTGCGCTGCTGCGCTGCTGCGCGCGCGCTGCTGCGCGCG 1667  
Db ACCGCGCGGATGCGCTCTGCGCTGCTGCGCTGCTGCGCGCGCGCTGCTGCGCGCG 100  
QY 1668 CCACCGCGCTCCCGCGCGCGCGCGCGAGACCGGAGAGCGCGCGCGCTGTGACCGCG 1727  
Db CCACCGCGCTCCCGCGCGCGCGCGCGAGACCGGAGAGCGCGCGCGCTGTGACCGCG 40  
QY 1728 GAATGCGCGCGCGCGCGCGCGCGCGCGAGTGGCGCGCTGCGCT 1766  
Db GAATGCGCGCGCGCGCGCGCGCGCGCGAGTGGCGCGCTGCGCT 1  
RESULT 13  
AB047147  
ID AB047147 standard; DNA; 1179 BP.  
XX  
AC AB047147;  
XX  
DT 12-JUL-2002 (first entry)  
XX  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33738.  
XX  
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200218632-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 01-SEP-2001; 2001WO-EP010074.  
XX  
PR 01-SEP-2000; 2000DE-01043826.  
XX  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX  
DR WPI; 2002-371829/40.  
XX  
PT Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation

CC status of many C residues to be determined simultaneously. ABQ13410-  
 CC ABQ1412 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention

XX Sequence 1179 BP; 399 A; 443 C; 159 G; 178 T; 0 U; 0 Other;

Query Match 24.8%; Score 761.4; DB 6; Length 1179;  
 Best Local Similarity 77.9%; Pred. No. 2.7e-117;  
 Matches 918; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

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Db 61 TCCTATAACCAAACTATCTATAATACAAATCATGCTCACGGAACCGAATAAAACTGT 120
Qy 708 CGCTAAGGGGCGCGGATTCCTCACTAGTGAAGAGGGAAGCCGCTTGAACCTGATGGC 767
Db 121 CGTAAACCGCCGAAATATTCATTAATAAAAAAAGCCCTTAAACTATCAATAAAC 180
Qy 768 CCGGAGAGGCGCGGAGGAGCGAGCATGCGCGGCGCGGAGCGCGGCGCTGGGCG 827
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Db 241 AAATTAACCGCGAACTAACTGAAAACCGCTGAAAACCCACCCGCAAAACCGCTTTCG 300
Qy 888 GCCCGGAGGAGCGAGCGAGCGCTCCGCGTGTGACCTGCGCGCGCGAGCGTGGGCGT 947
Db 301 GCCCGGAGGAGCGAGCGAGCGCTCCGCGTGTGACCTGCGCGCGCGAGCGTGGGCGT 360
Qy 948 GGGAAAGAGCGCTTACCGAGAGGAGCAACGCGCGAAGCTCCAGCCCGAGCCGAGAG 1007
Db 361 AAAAAAAACCGCTTACCGAAAAAACAACGCGCGAACTCCGAAACCGGCGAAACG 420
Qy 1008 CCGGCGCGCGGAGAGACCATGGGAGCCCTTGGAGCGGAGCGGAGCGGCGGAGG 1067
Db 421 CGAGGACCGCGGAGAACCATTAATAACCCCTTAAACGAAACGCGCGCGGAAAA 480
Qy 1068 GCGCGGAGGCGCGGCGCGCGCGCGCGCTTGGAGAGCGGCGCGCTGCGCCCTT 1127
Db 481 ACAGGAAAAACCGCGGTAAACCGCGCTTACCGCTTAAGAGAAAGCGCGTAACTGCGCTT 540
Qy 1128 CCCCTGGGGGCGCTGTGCGGTGACCGCGTGTGCTGTGCTGTGCTGTGCTGTG 1187
Db 541 CCCCTAAAAACGCTAATACGATACCGATACCGCTATATCTATCTATCTGTGCGAATA 600
Qy 1188 AGCGGCAACGTGTGACCGGTATGATGGGCGCTACCGGGAATGAGGACACAC 1247
Db 601 AAGGACAAGCTAATACCGTAACTATGATGAAACGCTACGAAACATGAAACACAC 660
Qy 1248 AACTTGTACTGGGAGACATGCGCGTGTGCGACTTACTATCTGTGCGGGTGCCTT 1307
Db 661 AACTTTATCTAAACAAATACCATACCGTATCGACTCTATCTATCTCAATACCGTTC 720
Qy 1308 GACCTGTACCGCTTGGCGCTGCGGCGCGCTGGGATTTGGGGCGGTGCTGCGCGCTG 1367
Db 721 GACTTATACCGCTTGAAGCTGCGACCTTAATTTGAAACCGCTACTTACGCGCTA 780
Qy 1368 TCCCTTACGTGGGCGAGGAGCTGACCTTACGCGACGCTGTGCAATGACCGCGCTAC 1427
Db 781 TCCCTTACGTAAACGAAACCTACCTACGCGACGCTACTACTACATACCGCGCTAAC 840
Qy 1428 GTGAGGCGCTACTGCGCATCTGGCGCGCGCTCCGCGCGCGCGGTGTGCTACCGGGGC 1487
Db 841 GTGAGGCGCTACTGCGCATCTGGCGCGCGCTCCGCGCGCGGTGTGCTACCGGGGC 900
Qy 1488 GCGGTCCGCGCGCTACGCTGTGCTGTGCGCGCGTGTGCTGTGCGCGGCTCTTC 1547

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Db 901 CGCGTCCGCGCGCTCATGCTATCTAATAACCGTAACGCTACTCTTACCGATCCCTTC 960
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Db 961 TTATTCCTAATAAAGCTGTGAACAAACCCGACATCTCGTAATCCGAACTCAATAAAC 1020
Qy 1608 ACCGCGGAGATGCGCTCTCTGCGCTCTGCGCTGTGCGCGGCTCTGTGCTCTCGCGGCG 1667
Db 1021 ACCGCGGAGATGCGCTCTCTGCGCTCTGCGCTGTGCGCGGCTCTGTGCTCTCGCGAAGC 1080
Qy 1668 CCAACCGCGTCCCGCGCGTCCGAGACCGCGAGAGCGCGGCGGCTGTCAAGCCGC 1727
Db 1081 CCACCGCGGTCCCGCGCGTCCGAAACCCGAAACCGGAAACCGGAGCGCTATTCAACCGC 1140
Qy 1728 GAATGCCGCGAGGCGCGCGAGCTGGGCGGCTGT 1766
Db 1141 GAATACGACCGAACCAGCCCGCGCACTAAGCGCTACGT 1179

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#### RESULT 14

ABQ47149/C  
 ID ABQ47149 standard; DNA; 1179 BP.

AC ABQ47149;

DT 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33740.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

KW drug; side effect; cancer; central nervous system; cardiovascular;

KW gastrointestinal; respiratory system; single nucleotide polymorphism;

XX SNP; cell differentiation; ds.

OS Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP010074.

PR 01-SEP-2000; 2000DE-01043826.

PP 05-SEP-2000; 2000DE-0104543.

PA (EPIC-) EPICENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K, Gnetig D;

DR WPI, 2002-371829/40.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation

status of many C residues to be determined simultaneously. AB013410-  
CC AB054121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
CC  
XX  
SQ Sequence 1179 BP; 462 A; 419 C; 159 G; 139 T; 0 U; 0 other;  
Query Match 23.5%; Score 722; DB 6; Length 1179;  
Best Local Similarity 75.8%; Pred. No. 9,2e-111;  
Matches 893; Conservative 0; Mismatches 285; Indels 0; Gaps 0;  
QY 589 AGATCCCTTGAAAGTGTCCCGAGTACCAAGTACAAAGCCCGGTACAGTCTCAGT 648  
DB 1178 AGATTTTTCGAAGGTGTCCGAGTATTAGATGAATAAAGCGTTCCGTATAGTTCAGT 1119  
QY 649 CCGTACCAAGGTGTCTAGGGTGCAGACATGCTACCGGACCGGGGTAGGGCTGTGC 708  
DB 1118 TTTGTAAATTAAGTGTGTTAGGGTGTAGATATATCTTTATCGATCGGATAGGGTGTGC 1059  
QY 709 GCTAAGGCGCCGCGGTATTCAGTTAGTGAAGAGGAGCGCCCTGAGACTGATGAGCC 768  
DB 1058 GTTAAAGGCGCGCGGTATTTAGTTAGTGAAGAGGAGCGTTTGGAAATTTGATGGGTT 999  
QY 769 CGGAGAGAGGGGCGGGAGCGGAGCATGCGCGGGCGGGGCGCGCGCGGTGGCGGA 828  
DB 998 CGGAGAGAGGGGCGGGAGCGGAGTGGGTGGGTGGGGCGCGGTGGGTGGGGCGGA 939  
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DB 938 GATTGCGCGTATAGTATTCGGAGCGTTCGAGTATTTTCGATAGAGTGTGTTTCGCG 879  
QY 889 CCGCGAGCGAGCGGAGCGGTCCGCGCTGATCTCCCGCGCGCGAGCGTGGCGGCTG 948  
DB 878 TTTGTATCGTACGATGCGTATGCGTGTGTTGATTTTCGCGTTCGATAGGAGTGGCGGTTG 819  
QY 949 GGAAGAGAGCGCTCAACGAGAGAGGAGCAACGCGCGAGCGTCCGAGCCCGAGCGCG 1008  
DB 818 GGAAGAGAGCGCTTATCGAGAGGAGATTCACCGTTAGGTTTATTTGTTGATTCGAGAGCG 759  
QY 1009 GCGCGCGCGCGGAGCAACCATGAGCGCCCTGGAACGAGAGCGAGCGCGCGAGGAG 1068  
DB 758 GCGCGTGGCGCGGAGTATTTATGCGTATTTTGAACGAGTATTCGATTCGAGGAGG 659  
QY 1069 CCGCGAGAGCGCGCGCGCGCGCGCTTCGCGTTCGAGAGCGCGCGCTGCTCGCGCTTC 1128  
DB 698 CCGCGAGTGTGTGTGTTGCGTGTGTTTCGAGAGCGCGTGTGTTGTTT 639  
QY 1129 CCTGAGGCGCGTGTGCGCGTGAACGCTGTGCTGCTGCTGCTGCTGCGGAGTGA 1188  
DB 638 TTTTGGGGCGCTTGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 579  
QY 1189 GCGGCAACGTGTGACCTGTATGCTATCGGGCGCTACCGGAGATGCGGACCA 1248  
DB 578 GCGGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 519  
QY 1249 ACTGTACCTGAGGAGCATGAGCGCGTCCGACTACCTACCTGCTGCGGCTGCGGTTG 1308  
DB 518 ATTGTATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 459  
QY 1309 ACTGTACCGCTGTGCGCTGCGCGCGCGCTGCGGCTGCGGCTGCTGCTGCGGCTGT 1368  
DB 458 ATTGTATGCTTTTGGCGCTTGGCGGTTTGGGATGCGGCTGCTGCTGCTGCTGCTGCT 399  
QY 1369 CCGCTACGTGGGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 1428  
DB 398 TTTTATGATGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 339  
QY 1429 TCGAGCGCTACCTGAGCTGCGCGCGCGCTGCGGCGCGCGCTGCTGCTGCTGCTGCTG 1488  
DB 338 TCGAGCGCTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 279  
QY 1489 GCGTCCGCGCGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548

DB 278 GCGTCCGCGCGTATTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 219  
QY 1549 TGTTCCTGTTGGGCGGTGAG 1608  
DB 218 TGTTCCTGTTGGGCGGTGAG 159  
QY 1609 CCGCGAGATGCGCTTCCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1668  
DB 158 TCGCGCGAGTGTGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCG 99  
QY 1669 CACGCGCGTCCCGCGCGTGGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1728  
DB 98 TATCGTGTGTTTTCGTTGCGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39  
QY 1729 AATGCGCGAG 1766  
DB 38 AATGTCGTGAGTGTGCGGTAGTTGGCGGCGGTTGCT 1  
RESULT 15  
AB047148  
ID AB047148 standard; DNA; 1179 BP.  
XX  
AC AB047148;  
XX  
DT 12-UTL-2002 (first entry)  
XX  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33739.  
XX  
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
XX Homo sapiens.  
XX  
PN MO200218632-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 01-SEP-2001; 2001MO-EP010074.  
XX  
PR 01-SEP-2000; 2000DE-01043826.  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
PA (EPIC-) EPIDENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX  
XX WPI; 2002-371829/40.  
PT Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
XX  
PS Claim 12; 56bp + Sequence Listing; 56bp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
XX genomic sample of DNA. The sample is treated chemically to convert in a  
XX cytosine (C) but not methylated C, to uracil, then part of the genomic  
XX DNA that contains the target C is amplified to form a labeled amplicon.  
XX The amplicon is hybridized to two classes, each with at least one member,  
XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
XX degree of hybridization to both classes is determined from the label on  
XX the amplicon. From the ratio of labels hybridized to the two classes of  
XX oligomers, the degree of methylation is calculated. The method is used:  
XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
XX and of a wide range of diseases, e.g. cancer, disorders of the central  
XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
XX particularly by detecting mutations or single nucleotide polymorphisms  
XX (SNPs); and (ii) for differentiation of cell or tissue types and for  
XX investigating cell differentiation. The method allows the methylation

CC status of many C residues to be determined simultaneously. AB013410-  
 CC AB054121 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention  
 CC  
 XX

Sequence 1179 BP; 139 A; 159 C; 419 G; 462 T; 0 U; 0 Other;

Query Match 23.5%; Score 722; DB 6; Length 1179;  
 Best Local Similarity 75.8%; Pred. No. 9.2e-111;  
 Matches 893; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

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QY 589 AGATCCCTCGAAGGTGCGCGAGTACAGACTGACAAAGCCGCCCTACAGTGCAGT 648
Db 2 AGATTTTTCGAAGGTGCGCGAGTATTAAGTATGATTAAGCCGTTCGTATAGTGTAGT 61
QY 649 CCTGTACCAAGCTGCTCTAGAGGTGACAGATGCTCAACGACCGGGTATGCGTCTGC 708
Db 62 TTGTGATTAAGTGTGTTAGGGGTGATATCGATATCGATCGGGTATGCGTCTGC 121
QY 709 GCTAAGGGCGCGGGGTATTCAGTTAGTGAAGAGGAAAGCCCTGAACTGCATGAGGCG 768
Db 122 GTTAAAGGCGGTGCGGTATTTTATGTTAGTGAAGAGGAAAGCGTTTGAATTTATAGGTT 181
QY 769 CGGAGAGGGCGCGGAGCGGAGCATGCGGGCGGGCGGGCGCGCGCGCTGCGGCGGA 828
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QY 829 GACTGCGCGAGTACGTGCGGAGCGGCTGCGAGCCCAACCCCGACAGCGCTTCTCGCG 888
Db 242 GATTGCGCGTATGTTAGTTCGAGAGCGTTTTCGAGATTATTTTCGTAAGTGTGTTTCGCG 301
QY 889 CCCCAGCGCAGCGCAGCGCTCCGCGTCTGACCTGCGCGCCCGCAGCGTTCGCGGCTG 948
Db 302 TTTCTAGCGTAGGCTGAGCGCTTTCGTGTTGATTTGTGCGCTTCGTAAGCGTTCGCGGTTG 361
QY 949 GAAAGAGAGCGCTCAACCGAGAGGACACAGCGCGCCGACCCCGACCGCGGAGCGC 1008
Db 362 GAAAGAGAGCGCTTATCGAGAGGAGTACGCGCTTATGTTGATTCGAGTTCGAGCGC 421
QY 1009 GAGGCGCGCGGAGGACCCATGAGGAGCGCCCTGGAACGAGCGACGCGCCCGAGGAGG 1068
Db 422 GCGGCTGCGCGGAGTATTTATGCGTATGTTTGGAAACGATGAGTTCGAGGAGG 481
QY 1069 CGCGGAGCGCGCGTGCCTGCGCGCTGCGCGCTTGGACAGAGCGCGCTGCGCGCTTTC 1128
Db 482 CGCGGAGCGTGTGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTTC 541
QY 1129 CCGTGGGCGCGCTGCTGCGCGTGAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1188
Db 542 TTTTGGGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
QY 1189 GCGGCAACGTGTGACCGTGTATGCTAGCGGCGCTACCGGAGCATGCGGACACACCA 1248
Db 602 GCGGTAAAGTGTGATCGTGTATGATCGGCGGTATCGGATATGCGGATTTATTTA 661
QY 1249 ACTTGTACCTGCGGACAGATGCGCGTGTGCGACTCATCTGCTGCGGCTGCGCTTCG 1308
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QY 1309 ACCGTGACCGCTCTGCGCGCTGCGCGCGCTGCGGCTTTCGCGCGCTGCTGCGCGCTG 1368
Db 722 ATTTGTATGCTTTTGTGCGCTGCGCGCTTTCGCGGCTGCGGCTGCTGCTGCTGCTG 781
QY 1369 CCTCTACGTGCGGCGGAGGTGACCTACGACAGCTGCTGACATGACCGGCTGACGCG 1428
Db 782 TTTTAAAGTGTGAGGAGGTGATTTATTAAGTATGATGATGATGATGATGATGATGATG 841
QY 1429 TCAGAGCTACCTGAGCATGCGCGCGCGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTG 1488
Db 842 TCAGAGCTATTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
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Db 902 GCGTCCGCGCTTATCGTGTGTTTGGGTGCGGCGTGTGTTTGTGCGTTCGTTTTC 961
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Db 962 TGTTCCTGTGTGCGCTCGAGCAGACCCCGCATCTCGTAGTCCCGGCGCTCAATGGCA 1021
QY 1609 CCGCGCGATGCGCTCTGCGCTGCTGCGCTGCTGCGCTGCTGCGCTGCTGCGCTGCTG 1668
Db 1022 TCGCGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1081
QY 1669 CACGCGCTCCCGCGCTGCGGAGCGAGACCGGAGCGCGCGCGCTGTCAGCGCG 1728
Db 1082 TATGCTGCTTTCGCTGCTGCGGAGTTCAGATCGCGGAGTTCGCGGCTGCTGCTGCTG 1141
QY 1729 AATGCGCGCAGCCCGCGCAGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1766
Db 1142 AATGCGCGCAGCTTTCGCGGAGTTCGCGGAGTTCGCGGCTGCTGCTGCTGCTGCTG 1179

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	234.8	7.7	1063	3	US-09-077-675A-1
6	234.8	7.7	1063	4	US-09-077-674-1
7	231.6	7.6	1095	4	US-09-743-475-2
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15	228.4	7.4	1092	4	US-09-077-674-15
16	228.4	7.4	3129	4	US-09-077-675A-14
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21	227.8	7.4	1101	4	US-09-170-496D-87
22	227.8	7.4	1101	4	US-09-170-496D-209
23	227.8	7.4	1101	4	US-09-364-425B-44
24	202.2	6.6	29629	4	US-09-729-995-3
25	202.2	6.6	29629	4	US-10-135-689-3
26	191.8	6.3	11282	4	US-09-758-250-3
27	191	6.2	152331	3	US-09-128-135-16

C 28	189.8	6.2	55298	4	US-09-491-356C-1	Sequence 1, Appl1
C 29	188.4	6.1	1912	4	US-09-800-729-32	Sequence 32, Appl1
C 30	187.6	6.1	24707	4	US-09-740-027-3	Sequence 3, Appl1
C 31	185.6	6.1	38653	4	US-09-922-445-1	Sequence 1, Appl1
C 32	185.6	6.1	50000	4	US-09-146-053-4	Sequence 1, Appl1
C 33	185.6	6.1	162450	4	US-09-345-882-1	Sequence 7, Appl1
C 34	185.4	6.0	7676	2	US-08-451-777A-7	Sequence 7, Appl1
C 35	185.4	6.0	7676	2	US-08-451-778A-7	Sequence 7, Appl1
C 36	185.4	6.0	7676	2	US-08-998-208-7	Sequence 7, Appl1
C 37	185.4	6.0	7676	5	PCT-US95-06743-7	Sequence 7, Appl1
C 38	185	6.0	21721	4	US-09-269-938A-41	Sequence 41, Appl1
C 39	185	6.0	22976	4	US-09-269-939A-19	Sequence 19, Appl1
C 40	185	6.0	23187	4	US-09-499-522-1	Sequence 1, Appl1
C 41	185	6.0	128779	4	US-09-497-855A-38	Sequence 38, Appl1
C 42	184.8	6.0	1827	2	US-08-737-371A-3	Sequence 3, Appl1
C 43	184.8	6.0	1827	5	PCT-US95-05853-3	Sequence 3, Appl1
C 44	184.8	6.0	7130	3	US-09-056-105-31	Sequence 31, Appl1
C 45	184.8	6.0	11288	3	US-08-646-301A-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-08-993-088A-4  
Sequence 4, Application US/08993088A  
Patent No. 6287855  
GENERAL INFORMATION:  
APPLICANT: Tan, Carina  
APPLICANT: Sullivan, Kathleen  
TITLE OF INVENTION: GALANIN RECEPTOR GALT2 AND  
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,088A  
FILING DATE: 18-DEC-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/033,651  
FILING DATE: 27-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 19846  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 283 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...283  
OTHER INFORMATION: cDNA probe  
US-08-993-088A-4



Query Match 9.2%; Score 283; DB 3; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1234 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1293  
1 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 60  
QY 1294 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1353  
DB 61 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 120  
QY 1354 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1413  
DB 121 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 180  
QY 1414 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1473  
DB 181 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 240  
QY 1474 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1516  
DB 241 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 283

## RESULT 2

US-08-993-424B-4  
; Sequence 4, Application US/08993424B  
; Patent No. 6337206  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Carina  
; APPLICANT: Kolakowski, Lee F., Jr.  
; TITLE OF INVENTION: MOUSE GALANTIN RECEPTOR GALR2 AND  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/993,424B  
; FILING DATE: 18-DEC-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/033,851  
; FILING DATE: 27-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 19846NP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1958  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 283 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; NAME/KEY: Other  
; LOCATION: 1...283  
; OTHER INFORMATION: cDNA probe

US-08-993-424B-4  
Query Match 9.2%; Score 283; DB 4; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1234 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1293  
1 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 60  
QY 1294 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1353  
DB 61 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 120  
QY 1354 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1413  
DB 121 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 180  
QY 1414 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1473  
DB 181 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 240  
QY 1474 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 1516  
DB 241 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTCTATCTG 283

## RESULT 3

US-09-603-680-4  
; Sequence 4, Application US/09603680  
; Patent No. 6544753  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Carina  
; APPLICANT: Sullivan, Kathleen  
; TITLE OF INVENTION: GALANTIN RECEPTOR GALR2 AND  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/603,680  
; FILING DATE: 26-Jun-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/033,851  
; FILING DATE: 27-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 19846 CA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1958  
; TELEFAX: 732-594-4720  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 283 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other



? APPLICANT: Smith, Roy G.  
 ? APPLICANT: Van der Ploeg, Leonardus H. T.  
 ? APPLICANT: Howard, Andrew D.  
 ? APPLICANT: Zheng, Hui  
 ? APPLICANT: McKee, Karen Kulju  
 ? APPLICANT: Jiang, Michael M.  
 ? TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE  
 ? TITLE OF INVENTION: RECEPTOR

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; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-743-475-2

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Query Match      7.6%; Score 231.6; DB 4; Length 1095;
Best Local Similarity 68.8%; Pred. No. 3.8e-37;
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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QY 1120 GCGCCCTTCCCTGGGGGCGGTGCTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 1179
DB 104 CACTGTTCCCGCGCGCGCTGCTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 163
QY 1180 TCGGGGTGAGCGGCAAGTGTGACCGTGTGATCGGGCGTACCGGGACATGCGGA 1239
DB 164 TGGGCATCTGGGGCAACTGTCTACACATGCTGTGTGTCTCCGCTTCCGGAGCTGGCA 223
QY 1240 CCACCAACAATTGTACTGTGGGAGCATGTGGCGGTGTCCGACTTACTGTCTGTGGGC 1299
DB 224 CCACCAACAATTGTACTGTGGGAGCATGTGGCGGTGTCCGACTTACTGTCTGTGGGC 283
QY 1300 TGGCGTGGACCTGTACCGCGCTGTGGCGGTGTGGCGGTGTGGCGGTGTGGCGGTGT 1359
DB 284 TGGCGTGGACCTGTGTGCGCTGTGGCGGTGTGGCGGTGTGGCGGTGTGGCGGTGT 343
QY 1360 GCGCGCTGTCCCTGTACGTGTGGGCGGAGGCTGTGACCTGTGACCGCTGTGACATGACG 1419
DB 344 GCACACTCTTCAAGTTGTGACGAGAGCTGTGACCTGTGACCGCTGTGACATGACG 403
QY 1420 CGCTCAGCGTGAAGCGCTACTGTGGCGGCAATGCGCGCGGTGTGGCGCGGTGTGGTCA 1479
DB 404 CGCTCAGCGTGAAGCGCTACTGTGGCGGCAATGCGCGCGGTGTGGCGCGGTGTGGTCA 463
QY 1480 CCGGCGCGCGGTGTGGCGGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1539
DB 464 CCAAGGGCGGTGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 523
QY 1540 GTCCCTTCTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1581
DB 524 GGGCCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 565

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RESULT 8
US-09-743-475-1
; Sequence 1, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4009
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-743-475-1

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Query Match      7.6%; Score 231.6; DB 4; Length 4009;
Best Local Similarity 68.8%; Pred. No. 5.7e-37;
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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QY 1120 GCGCCCTTCCCTGGGGGCGGTGCTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 1179
DB 605 CACTGTTCCCGCGCGCGCTGCTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 664
QY 1180 TCGGGGTGAGCGGCAAGTGTGACCGTGTGATCGGGCGTACCGGGACATGCGGA 1239
DB 665 TGGGCATCTGGGGCAACTGTCTACACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 724
QY 1240 CCACCAACAATTGTACTGTGGGAGCATGTGGCGGTGTCCGACTTACTGTCTGTGGGC 1299
DB 725 CCACCAACAATTGTACTGTGGGAGCATGTGGCGGTGTCCGACTTACTGTCTGTGGGC 784
QY 1300 TGGCGTGGACCTGTGTGCGCGCTGTGGCGGTGTGGCGGTGTGGCGGTGTGGCGGTGT 1359
DB 785 TGGCGTGGACCTGTGTGCGCGCTGTGGCGGTGTGGCGGTGTGGCGGTGTGGCGGTGT 844
QY 1360 GCGCGCTGTCCCTGTACGTGTGGGCGGAGGCTGTGACCTGTGACCGCTGTGACATGACG 1419
DB 845 GCACACTCTTCAAGTTGTGACGAGAGCTGTGACCTGTGACCGCTGTGACATGACG 904
QY 1420 CGCTCAGCGTGAAGCGCTACTGTGGCGGCAATGCGCGCGGTGTGGCGCGGTGTGGTCA 1479
DB 905 CGCTCAGCGTGAAGCGCTACTGTGGCGGCAATGCGCGCGGTGTGGCGCGGTGTGGTCA 964
QY 1480 CCGGCGCGCGGTGTGGCGGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1539
DB 965 CCAAGGGCGGTGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1024
QY 1540 GTCCCTTCTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1581
DB 1025 GGGCCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1066

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RESULT 9
US-09-077-675A-4
; Sequence 4, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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CITY: Rahway  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 07065-0900  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatidle  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/077,674  
 FILING DATE: 3-JUN-1998  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cocuzzo, Anna L.

REFERENCE/DOCKET NUMBER: 19589P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1273

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? TELEX:
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1029 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? OS-09-077-674-4

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	Query Match	Best Local Similarity	7.5%; Score
	Matches	317; Conservative	0; Mismatches
QY	1120	CGCCCTTTCCCTCGGGGGCGCTG	266
DB	266	CGCTCTTCCACAGCGCGCTGTGGC	1180
QY	1180	TGCGGGTGAGCGGCAAGTGAGTGC	326
DB	326	TGGGTATCGGGGCAACTGCTCAC	1240
QY	1240	CCACCAACAATTGTACTTGGGACAG	386
DB	386	CCACCAACAACCTTCACTGTCCAG	1300
QY	1300	TGCGATTGACAGCTGACCGGCTCTG	446
DB	446	TGCCCTCGAAGCTTTCGCGCTTGG	1360
QY	1360	GCCGCTGTCTCCCTTACGTGGGCGA	

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QY      1420  CGCTGACGCTCGAGCGCTACTTGGCC
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Db      566  CGCTGAGCGTCCGAGCGCTACTTGGCC
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QY      1480  CCGGAGCGCGCGCTCCGCGCGCTCAT
          |||
Db      626  CCAAGGGCGGGGTAAAGCTGTGTCAT
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QY      1540  GTCCCTTCTTGTCTCTGATGAGGCGGT
          |||
Db      686  GGCCTCATCTTCGTGCTGTGTGGAGAT
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Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HERWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 359:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: THPINOT01  
CLONE: 2018536  
US-09-016-434-359

Query Match 7.5%; Score 229; DB 4; Length 250;  
Best Local Similarity 98.8%; Pred. No. 7.7e-37;  
Matches 240; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
DB 1 TCTGAGTACTTAATGATGCTGCTGCACTTTCTATCTGAGCGCATCAACCA 2883  
QY 2884 ATCTCTAACACCTTCATTTCAAAGAGTACAGAGCGCGGCTTTAAATGCTGCTGCA 2943  
DB 61 ATCTCTAACACCTTCATTTCAAAGAGTACAGAGCGCGGCTTTAAATGCTGCTGCA 120  
QY 2944 AGAAGTCCAGGCGAGGAGGCTTCCACAGAGGAGGAGCACTGGGGGGGAAGTGGACGG 3003  
DB 121 AGAAGTCCAGGCGAGGAGG- TTCCACAGAGGAGGAGCACTGGGGGGGAAGTGGACGG 179  
QY 3004 GACACTGAGAGACACCGGTGGGTACACCGAGACAAACCGCTAAAGTAAAGCATGGGA 3063  
DB 180 GACACTGAGAGACACCGGTGGGTACACCGAGACAAACCGCTAAAGTAAAGCATGGGA 239  
QY 3064 TAA 3066  
DB 240 TAA 242

Patent No. 6242199  
GENERAL INFORMATION:  
APPLICANT: Pai, Lee-Yuh  
APPLICANT: Feisner, Scott C.  
APPLICANT: Howard, Andrew D.  
APPLICANT: Pong, Sheng-Shung  
APPLICANT: Van Der Ploeg, Leonardus H.T.  
TITLE OF INVENTION: RECEPTOR ASSAY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/077,675A  
FILING DATE: 3-JUN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cocuzzo, Anna L.  
REGISTRATION NUMBER: 42,452  
REFERENCE/DOCKET NUMBER: 19590P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1273  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1122 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-077-675A-9

Query Match 7.5%; Score 228.8; DB 3; Length 1122;  
Best Local Similarity 57.9%; Pred. No. 1.4e-36;  
Matches 424; Conservative 0; Mismatches 307; Indels 1; Gaps 1;  
DB 1121 GCGCTTCCCGCGGGGCGCTGTCACCGGTGACCGCTGTGCTGTGCTGTGCTGT 1180  
QY 360 GCGCTTCCCGCGGGGCGCTGTCACCGGTGACCGCTGTGCTGTGCTGTGCTGTGCT 419  
DB 1181 CGGGTGAAGCGGCAAGTGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 1240  
QY 420 GGGTATCGGTGCAACCTGCTCAACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 479  
DB 1241 CACCAACAATTGTACTGGGAGAGATGAGCGGCTGTCCGACTACTACTACTCTCTGGGCT 1300  
QY 480 CACCAACAATTGTACTGGGAGAGATGAGCGGCTGTCCGACTACTACTACTCTCTGGGCT 539  
DB 1301 GCCGTTCAGCTGTACCGGCTCTGCGCGCTGCGCGGCTGTGGGTGTGTGTGTGTGTGT 1360  
QY 540 GCCCTTCAGCTGTACCGGCTCTGCGCGCTGCGCGGCTGTGGGTGTGTGTGTGTGTGTGT 599  
DB 1361 CGGCTGTCCCTCTAGTGGGAGAGGCTGACCTAGCGGCAAGCTGTGCTGACATGACGCG 1420  
QY 600 CAACTCTTCCATTGTGTGAGTGAAGCTGCACTAGCGGCAAGCTGTGCTGACATGACGCG 659  
DB 1421 GCTCAGCGTGAAGCGCTACTGAGCATCTGCGCGCGCTGCGCGCGCGCTGTGTGTGTGT 1480  
QY 660 GCTCAGCGTGAAGCGCTACTGAGCATCTGCGCATGTGCTTCCATCCCGGCGCAAGGTGTGTGTGT 719







Db 344 GCAAACTTTTCCAGTTTGTACGAGAGCTGCACTACGCCACGGTCTCACCATCACCG 403  
QY 1420 CGCTCAGCGTCGAGCGCTACCTGAGCCATCTGCCCCCGCTCCGGCCCCGCGCTTGGTCA 1479  
Db 404 CGCTGAGGCTCGAGCGGCTACTTGGCACTGCTTCCCTCTGCGGGCCAGGTGGTCA 463  
QY 1480 CCGGCGCGCGCTCCGGCGCTCATCGCTGTGCTTGGGCCGTGGCGCTGCTCTTGCCG 1539  
Db 464 CTAAAGGCGCGGTAAGCTGTATCTTGTATCTGGGCCGTGGCTTTCTGACGCGCG 523  
QY 1540 GTCCCTTCTTGTCTGAGGCGCTGAGCAGAGACCCGCGCA 1581  
Db 524 GGGCCATCTTGTGTGTGGCGCTGAGACACGAAGCGCA 565

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Job time : 210 secs

Thu Jul 22 08:37:31 2004

us-09-719-485-1.rmpb

Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 16:34:38 ; Search time 1291 Seconds

(without alignments)  
11586.258 Million cell updates/sec

Title: US-09-719-485-1

Perfect score: 3066

Sequence: 1 ttgaatatctgtcactg.....acgtgaagacgatggataa 3066

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3190992 segs, 2439311697 residues 6381984

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2021.2	65.9	2040	13	US-09-876-252-129
2	2021.2	65.9	2040	16	US-10-417-820A-129
3	2021.2	65.9	2040	17	US-10-723-955-129
4	2013.2	65.7	2040	16	US-10-417-820A-151
5	2013.2	29.4	1239	15	US-10-235-567A-472
6	901	29.4	1239	15	US-10-280-078-13
7	901	29.4	1239	15	US-10-280-078-14
8	901	29.4	1239	15	US-10-206-677-1
9	234.8	7.7	1063	15	US-10-303-204A-1
10	230	7.5	1029	15	US-10-303-204A-4
11	229	7.5	250	16	US-10-305-720-359
12	228.8	7.5	870	15	US-10-225-567A-139
13	228.8	7.5	1122	15	US-10-303-204A-9
14	228.4	7.4	1092	15	US-10-303-204A-15

15	228.4	7.4	3129	15	US-10-303-204A-14	Sequence 14, Appl
16	227.8	7.4	1088	15	US-10-303-204A-6	Sequence 6, Appl
17	227.8	7.4	1101	15	US-10-251-385-87	Sequence 87, Appl
18	227.8	7.4	1101	15	US-10-251-385-209	Sequence 209, Appl
19	227.8	7.4	1101	15	US-10-276-392-22	Sequence 22, Appl
20	227.8	7.4	1101	16	US-10-305-720-1148	Sequence 1148, Ap
21	205.2	6.7	5157	9	US-09-764-877-2605	Sequence 2605, Ap
22	205.2	6.7	5157	16	US-10-242-515-2605	Sequence 2605, Ap
23	205.2	6.7	5199	16	US-09-764-877-2607	Sequence 2607, Ap
24	205.2	6.7	5199	16	US-10-242-515-2607	Sequence 2607, Ap
25	202.2	6.6	29629	14	US-10-135-689-3	Sequence 3, Appl
26	202.2	6.6	29629	17	US-10-690-617-3	Sequence 3, Appl
27	201.8	6.6	12822	9	US-09-764-847-1579	Sequence 1579, Ap
28	201.8	6.6	12822	15	US-10-092-154-1579	Sequence 1579, Ap
29	201.2	6.6	953	13	US-10-027-632-248867	Sequence 248867, Ap
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31	200.8	6.5	704	13	US-10-027-632-125989	Sequence 125989, Ap
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33	200.4	6.5	39768	13	US-10-087-192-1030	Sequence 1030, Ap
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38	200	6.5	39148	13	US-10-087-192-46	Sequence 46, Appl
39	199.8	6.5	1920	16	US-10-094-749-198	Sequence 198, Appl
40	199.6	6.5	704	13	US-10-027-632-125890	Sequence 125890, Ap
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44	199.6	6.5	704	16	US-10-027-632-125991	Sequence 125991, Ap
45	199.6	6.5	704	16	US-10-027-632-125992	Sequence 125992, Ap

RESULT 1  
US-09-876-252-129  
Sequence 129, Appl  
Publication No. US20030018182A1  
GENERAL INFORMATION:  
APPLICANT: Behan, Dominic P.  
APPLICANT: Lehmann-Bruinsma, Karin  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Lowitz, Kevin P.  
APPLICANT: Lin, I'-lin  
APPLICANT: Dang, Huong T.  
APPLICANT: Chen, Ruoping  
APPLICANT: Liaw, Chen W.  
TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Re  
FILE REFERENCE: AREN-0054  
CURRENT APPLICATION NUMBER: US/09/876,252  
CURRENT FILING DATE: 2001-06-07  
PRIOR APPLICATION NUMBER: 09/416,760  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: 09/170,496  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: 60/110,060  
PRIOR FILING DATE: 1998-11-27  
PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,852  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/109,213  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: 60/123,944  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,945  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,948  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,951  
PRIOR FILING DATE: 1999-03-12

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1  / PRIOR APPLICATION NUMBER: 60/123,946
2  / PRIOR FILING DATE: 1999-03-12
3  / PRIOR APPLICATION NUMBER: 60/123,949
4  / PRIOR FILING DATE: 1999-03-12
5  / PRIOR APPLICATION NUMBER: 60/152,524
6  / PRIOR FILING DATE: 1999-09-03
7  / PRIOR APPLICATION NUMBER: 60/151,114
8  / PRIOR FILING DATE: 1999-08-27
9  / PRIOR APPLICATION NUMBER: 60/108,029
10 / PRIOR FILING DATE: 1998-11-12
11 / PRIOR APPLICATION NUMBER: 60/136,436
12 / PRIOR FILING DATE: 1999-05-28
13 / PRIOR APPLICATION NUMBER: 60/136,439
14 / PRIOR FILING DATE: 1999-05-28
15 / PRIOR APPLICATION NUMBER: 60/136,567
16 / PRIOR FILING DATE: 1999-05-28
17 / PRIOR APPLICATION NUMBER: 60/137,127
18 / PRIOR FILING DATE: 1999-05-28
19 / PRIOR APPLICATION NUMBER: 60/137,131
20 / PRIOR FILING DATE: 1999-05-28
21 / PRIOR APPLICATION NUMBER: 60/141,448
22 / PRIOR FILING DATE: 1999-06-29
23 / PRIOR APPLICATION NUMBER: 60/136,437
24 / PRIOR FILING DATE: 1999-05-28
25 / PRIOR APPLICATION NUMBER: 60/156,555
26 / PRIOR FILING DATE: 1999-09-29
27 / PRIOR APPLICATION NUMBER: 60/156,634
28 / PRIOR FILING DATE: 1999-09-29
29 / PRIOR APPLICATION NUMBER: 60/156,653
30 / PRIOR FILING DATE: 1999-09-29
31 / PRIOR APPLICATION NUMBER: 60/157,280
32 / PRIOR FILING DATE: 1999-10-01
33 / PRIOR APPLICATION NUMBER: 60/157,294
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37 / PRIOR APPLICATION NUMBER: 60/157,282
38 / PRIOR FILING DATE: 1999-10-01
39 / PRIOR APPLICATION NUMBER: 60/156,633
40 / PRIOR FILING DATE: 1999-09-29
41 / NUMBER OF SEQ ID NOS: 146
42 / SOFTWARE: PatentIn version 3.0
43 / SEQ ID NO 129
44 / LENGTH: 2040
45 / TYPE: DNA
46 / ORGANISM: Homo sapiens
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QY	1149	GTAACCGCTGTGTGCTCTGTGCTTGTCTGCTGGGGGTGAACGGCAAGTGTACCGTG	1208	
Db	121	GTAACCGCTGTGTGCTCTGTGCTTGTCTGCTGGGGGTGAACGGCAAGTGTACCGTG	180	
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Db	181	ATGCTGATTCGGGCGCTACCGGGAGATGCGACCAACCAACTTGTACTCTGGGAGCATG	240	
QY	1269	GCGGTGACCGACCTACTCATCTCTGCTGGGCTGCGGCTTCAGACCTGTACCGCTTGGCGC	1328	
Db	241	GCGGTGACCGACCTACTCATCTCTGCGGCTGCGGCTTCAGACCTGTACCGCTTGGCGC	300	
QY	1329	TTCGCGCCCTTGGGTGTTGGGGCGCTGCTTGC CGCTTATCCCTTCAAGTGTGGGAGAGGC	1388	

Db	301	TCGGGGCCCTGGAGTGTTCGGGGCCGCTGCTCTGCGCCCTGTCCCTTACGTGGAGCGAGGGC	360
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Qy	1449	TGCGCCGCCGCTCCGGGCCCGCGCTCTTGGTACCCGGGCGCGCGTCCGCGGCTCATGCT	1507
Db	421	TGCGCCGCCGCTCCGGGCCCGCGCTCTTGGTACCCGGGCGCGCGTCCGCGGCTCATGCT	480
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Qy	1569	CAGAACCCCGGATCTCCGTAGTCCCGGGCTCATGACCCGCGGGATGCGCTTCTCG	1622
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Qy	1629	CCCTCTGCGCTGCGCGCGCTCTCTCTGAGTCTCGGGGCGGACACCGCGTCCCGCGCTGCG	1688
Db	601	CCCTCTGCGCTGCGCGCGCTCTCTCTGAGTCTCGGGGCGGACACCGCGTCCCGCGCTGCG	660
Qy	1689	GAGGCCCGGAGACCGCGAGGCGCGCGCGCTGTTACCGCGCATGCGGCGGACCCCGCG	1746
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Qy	1749	CAGCTGGGCGCGCTGCGTATCTGTGGGTACACACCGCCCTACTTCTTCTGCGCTT	1807
Db	721	CAGCTGGGCGCGCTGCGTATCTGTGGGTACACACCGCCCTACTTCTTCTGCGCTT	780
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Qy	1869	CTGCGAGGCGCGCGCTCTGGGAGCGGAGAGAGCCACCGCGACACGCTCGCGTCTG	1922
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Qy	1929	CGTAAATGAGACCGCGCTGTTCACAAAGACGCTGACGTCCGCGCCCGCGCGAGAC	1988
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Qy	1989	GCGCAACGCTGGGTCCCTTCCCTGCTCGCCACGCTGGGCGCGCTTCAGCTCC	2048
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Qy	2049	--TCCATTATGATTCACAGCTCCACCGCGCGGATCTCCACATCCCGCGAGAAACGATG	2106
Db	1021	TTTTCATTATGATTCACAGCTCCACCGCGCGGATCTCCACATCCCGCGAGAAACGATG	1080
Qy	2107	TCTGTCCCGCAGAGACTCTGGGAGACCCGAGGCGCTTGAAGGTGGATCCCGGATC	2166
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Qy	2167	CGATTCACTAACAGCACTGCTTTCCAGACCTCTGAGACCAAGAAAGAGTTGGTAA	2222
Db	1141	CGATTCACTAACAGCACTGCTTTCCAGACCTCTGAGACCAAGAAAGAGTTGGTAA	1200
Qy	2227	TTCTTAATCCACACCGCTGATAGTGCACAAATGAGAGTCTTCACTGTCTTTGAGA	2286
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Qy	2287	AACACAGGAGATTTCACTAAAGCTAAATTTTATTAATGTTAACTGATCTGAGAGC	2346
Db	1261	AACACAGGAGATTTCACTAAAGCTAAATTTTATTAATGTTAACTGATCTGAGAGC	1320
Qy	2347	TAAAGTAAACCTGTGCTGATCAAAAAGTAAAGTTGTGCAGACCGTTGTGAGATTCCT	2406
Db	1321	TAAAGTAAACCTGTGCTGATCAAAAAGTAAAGTTGTGCAGACCGTTGTGAGATTCCT	1380
Qy	2407	TTCAAACAGAGAACAAAACCTGTCTTCGAGTGGGTTGTGAAAGAACCTGCGACG	2466

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Page 3

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QY	2647	GCAATAGTTCCTTGTCGGGGGTGGGGGGTTATTGCTGCCAGATGCTTTGTTAATCCC	2706
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QY	2707	GGTCTGTGTCTTATGTTGACAGTGGTGGTCTTGCACTTATATATTTGCTGGTGGCC	2766
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QY	2767	TTCCACGTTGGCAGAAATCATTTAACAATAACAGGAAGTTGCGGATGATGACTTCTCT	2826
Db	1741	TTCCACGTTGGCAGAAATCATTTAACAATAACAGGAAGTTGCGGATGATGACTTCTCT	1800
QY	2827	CAGAACCTTAAACATGTCGCTCTGCAACTTTTCATCTGAGCGGATCATATCAACCAATC	2886
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QY	2887	CTCTACAACCTCATTTTCAAAGAAATACAGACGGCGGCTTTAAACTGCTCTCGCAAG	2946
Db	1861	CTCTACAACCTCATTTTCAAAGAAATACAGACGGCGGCTTTAAACTGCTCTCGCAAG	1920
QY	2947	AAGTCCAGGCGGAGAGGCTTCCACAAGAAACAGGGAACACTGCGGGGGAAGTTGCAAGGGAC	3006
Db	1921	AAGTCCAGGCGGAGAGGCTTCCACAAGAAACAGGGAACACTGCGGGGGAAGTTGCAAGGGAC	1980
QY	3007	ACTGAGAGAGACAGGATGGGCTACACCGAGCAAGCGCTAACGTGAAGACGATGGGATTA	3066
Db	1981	ACTGAGAGAGACAGGATGGGCTACACCGAGCAAGCGCTAACGTGAAGACGATGGGATTA	2040

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1 RESULT 2
2 US-10-417-820A-129
3 Sequence 129, Application US/10417820A
4 Publication No. US20030229216A1
5 GENERAL INFORMATION:
6 APPLICANT: Chen, Ruoping
7 APPLICANT: Liaw, Chen W.
8 APPLICANT: Lowitz, Kevin
9 APPLICANT: Chaimers, Derek T.
10 APPLICANT: Behan, Dominic P.
11 TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
12 TITLE OF INVENTION: Receptors
13 FILE REFERENCE: 7 US28 CON
14 CURRENT APPLICATION NUMBER: US/10/417,820A
15 CURRENT FILING DATE: 2003-04-16
16 PRIOR APPLICATION NUMBER: 09/416,760
17 PRIOR FILING DATE: 1999-10-12
18 PRIOR APPLICATION NUMBER: 09/170,456
19 PRIOR FILING DATE: 1998-10-13
20 PRIOR APPLICATION NUMBER: 60/110,060
21 PRIOR FILING DATE: 1998-11-27
22 PRIOR APPLICATION NUMBER: 60/120,416
23 PRIOR FILING DATE: 1998-02-16
24 PRIOR APPLICATION NUMBER: 60/121,852
25 PRIOR FILING DATE: 1999-02-26
26 PRIOR APPLICATION NUMBER: 60/109,213
27 PRIOR FILING DATE: 1998-11-20
28 PRIOR APPLICATION NUMBER: 60/123,944
29 PRIOR FILING DATE: 1999-03-12
30 PRIOR APPLICATION NUMBER: 60/123,945

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[illegible]

QY	18639	TTGGGAGAGGC	CCGCGCCGCTTCGGGGG	GGGAGAGAGCCAC	CCGCGACACCGTCCGCGTCTG	19228
Db	841	CTGCGAGGCGCGGCGCGCTCGGGG	GGGAGAGAGGCGCAC	CCGCGACACCAAACGCGTCTTG		900
QY	19259	CGTAAGTGGAGCGCGCGTGGTTC	CAAAACGCTGCTCGAGTCCGCCCGCGGGAGC		19888	
Db	901	CGTAAGTGGAGCGCGCGTGGTTC	CAAAAGACGCTGCTCGAGTCCGCCCGCGGGAGC		960	
QY	19899	GGCGAAAGCGTGGGTCCCCCTT	CCCCGTGCGCCGACGCTCTGGGGCGCGCTTCAGCTGCC		20458	
Db	961	GGCGAAAGCGTGGGTCCCCCTT	CCCCGTGCGCCGACGCTCTGGGGCGCGCGCTTCAGCTGCC		10220	
QY	20449	--TCCATTTTCGATTC	CAACCTCCACCCGCGGACTTCCCATCCCCCGAGAAAACATG		21060	
Db	1021	TTTCCATTTTCGATTC	CAACCTCCACCCGCGGACTTCCCATCCCCCGAGAAAACATG		10808	
QY	2107	TCCGTGCCCCCAGGAGGCTCTG	GGGGAGCCCGAGGGCGCTTGAAGGCTGGGATCCCCGAGTC		21666	
Db	1081	TCCGTGCCCCCAGGAGGCTCTG	GGGGAGCCCGAGGGCGCTTGAAGGCTGGGATCCCCGAGTC		11400	
QY	2167	CGATTCAGTAAAC	CAGCAGTGCCTTTCCAGACCCCTCTG	AGACAGAAAGAGAGTGTGTA	22266	
Db	1141	CGATTCAGTAAAC	CAGCAGTGCCTTTCCAGACCCCTCTG	AGACAGAAAGAGAGTGTGTA	12000	
QY	2227	TTCTTAATCCACCAAC	CGCTGTGAAGTGGCAAAATGAGGAGTCCACAGTGCCTCTGA		22866	
Db	1201	TTCTTAATCCACCAAC	CGCTGTGAAGTGGCAAAATGAGGAGTCCACAGTGCCTCTGA		12600	
QY	2287	AGACGAGGAGATTC	ATTAAAGCTAAATTTTTTAATTTAATGTAAAGTATGCTGAAGGC		23466	
Db	1261	AGACGAGGAGATTC	ATTAAAGCTAAATTTTTTAATTTAATGTAAAGTATGCTGAAGGC		13200	
QY	2347	TAAAGTAAC	CGTGCCTGATCAAAABAATGTG	CAGACCTGTGTGAATACTT	24066	
Db	1331	TAAAGTAAC	CGTGCCTGATCAAAABAATGTG	CAGACCTGTGTGAATACTT	13800	
QY	2407	TTCAAACAGAGAA	CAGAAAATCTGTCTCCGAAGTGGGTTTGTGAAGAGCCTGSCAAG		24666	
Db	1381	TTCAAACAGAGAA	CAGAAAATCTGTCTCCGAAGTGGGTTTGTGAAGAGCCTGSCAAG		14400	
QY	2467	CGGCTGTGTGAGAAAT	TGCTCCTCGGTTATGTGCACGCTGTATCAACATATGGG		25266	
Db	1441	CGGCTGTGTGAGAAAT	TGCTCCTCGGTTATGTGTGCACGCTGTATCAACATATGGG		15000	
QY	2527	AGCCTACTATG	CAAGTTTAAANGCAAGTATCCATGCAAGCTGACAGCTGATCATTTTTCT		25866	
Db	1501	AGCCTACTATG	CAAGTTTAAANGCAAGTATCCATGCAAGCTGACAGCTGATCATTTTTCT		15600	
QY	2587	GGGGTAGAGAT	CTGCTCGATGATGAGAAGTTTCTTAATTTATTTTGCTGTATCTGTAAAT		26466	
Db	1561	GGGGTAGAGAT	CTGCTCGATGATGAGAAGTTTCTTAATTTATTTTGCTGTATCTGTAAAT		16200	
QY	2647	GCAAGTGTCTCTTGTG	GGGGGTGGGGGTTAATTTGCTTCCCAATGCTTTTGTAAATCC		27066	
Db	1621	GCAAGTGTCTCTTGTG	GGGGGTGGGGGTTAATTTGCTTCCCAATGCTTTTGTAAATCC		16800	
QY	2707	GGTGTGTGTATTAT	TGTGACAGTGTGGTCTCGGACATTAAATTTGCTGTGGTCC		27666	
Db	1681	GGTGTGTGTATTAT	TGTGACAGTGTGGTCTCGGACATTAAATTTGCTGTGGTCC		17400	
QY	2767	TTCCACGTTGGCAAAAT	CATTATTAACATTAACACGGAAGATTGCGGATGATGTACTTCT		28266	
Db	1741	TTCCACGTTGGCAAAAT	CATTATTAACATTAACACGGAAGATTGCGGATGATGTACTTCT		18000	
QY	2827	CAGACTTTAAACAT	GTGCTGCTCAACTTTTCTATCTGACGCGATCATCAACCAATC		28866	
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QY	2887	CTCTACAACCTGAT	TTTCAAAGAATCAGAGCGCGGCTTTAAATCTGCTGTGCAAG		29466	
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Qy      2947  AAGTCCAGCCGAGAGGCTTCCACAGAAAGCAGGGACACACTGGGGGGAAGTTGCAAGGGGAC  3008
Db      1921  AAGTCCAGCCGAGAGGCTTCCACAGAAAGCAGGGACACTGGGGGGAAGTTGCAAGGGGAC  1980

Qy      3007  ACTGAGGAGACACAGCGTGGGCTACACCGAGACAAGCGCTTAACTGAAGCAGTGGATTA  3066
Db      1981  ACTGAGGAGACACAGCGTGGGCTTACACCGAGACAAGCGCTTAACTGAAGCAGTGGATTA  2040

RESULT 3
US-10-723-955-129
; Sequence 129, Application US/10723955
; Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, I-Lin
APPLICANT: Liaw, Chen W.
APPLICANT: Lehman-Brulsma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
FILE REFERENCE: 7, US29, CON
CURRENT FILING DATE: 2003-11-26
PRIORITY FILING DATE: 2003-11-26
PRIORITY FILING DATE: 10/417, 820
PRIORITY FILING DATE: 2003-4-16
PRIORITY FILING DATE: 09/446, 760
PRIORITY FILING DATE: 1999-10-12
PRIORITY FILING DATE: 09/170, 496
PRIORITY FILING DATE: 1998-10-13
PRIORITY FILING DATE: 60/110, 060
PRIORITY FILING DATE: 1998-11-27
PRIORITY FILING DATE: 60/120, 416
PRIORITY FILING DATE: 1999-02-16
PRIORITY FILING DATE: 60/121, 852
PRIORITY FILING DATE: 1999-02-26
PRIORITY FILING DATE: 60/109, 213
PRIORITY FILING DATE: 1998-11-20
PRIORITY FILING DATE: 60/123, 944
PRIORITY FILING DATE: 1999-03-12
PRIORITY FILING DATE: 60/123, 945
PRIORITY FILING DATE: 1999-03-12
PRIORITY FILING DATE: 60/123, 948
PRIORITY FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 129
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-955-129

Query Match      65.9%; Score 2021.2; DB 17; Length 2040;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2035; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy      1029  ATGGGACAGCCCTTGGAAACGGCAGCAGCGCCCGAGGGGGCGGGGAGCCGCGTGGCCC  1088
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Qy      1089  GCGGTGACGCGCTTGGCGACGAGCGCCGCTGCTCCCTTTCCCTGGGGGAGCGCTGGTCCG  1148
Db      61      GCGGTGACGCGCTTGGCGACGAGCGCCGCTGCTCCCTTTCCCTGGGGGAGCGCTGGTCCG  120

Qy      1149  GTGACCGCTGTGTGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  1208
Db      121      GTGACCGCTGTGTGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  180

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QY 1209 ATGCTGATCGGCGCTACCGGGACATGCGACACCACTTGTACTTGGGAGCATG 1268  
 DB 181 ATGCTGATCGGCGCTACCGGGACATGCGACACCACTTGTACTTGGGAGCATG 240  
 QY 1269 GCGGTGTCGACCTACTACTTCTGCTGGGGTGGCGGTTCGACCTGTACCGCTCTGGCGC 1328  
 DB 241 GCGGTGTCGACCTACTACTTCTGCTGGGGTGGCGGTTCGACCTGTGTACCGCTCTGGCGC 300  
 QY 1329 TCGGCGCCTGGGTGTTGCGGCGCGCTGTGCGCGCTGTCCCTGTACTGTGGGCGAGGC 1388  
 DB 301 TCGGCGCCTGGGTGTTGCGGCGCGCTGTGCGCGCTGTCCCTGTACTGTGGGCGAGGC 360  
 QY 1389 TGCACCTACGCGACGCTGTGCAATGACCGCGCTCAAGCGTCAAGCGCTACTGGCCATC 1448  
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 QY 1449 TGGCGCGCGCTCGGCGCGCGGTGTGCTGCTGACCGCGCGCGCGGTGCGCGCGCTCATGCT 1508  
 DB 421 TGGCGCGCGCTCGGCGCGCGGTGTGCTGCTGACCGCGCGCGCGGTGCGCGCGCTCATGCT 480  
 QY 1509 GTGCTCTGGGCGGTGCGCGCTGTGCTGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTG 1568  
 DB 481 GTGCTCTGGGCGGTGCGCGCTGTGCTGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTG 540  
 QY 1569 CAGAACCCCGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1628  
 DB 541 CAGAACCCCGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 QY 1629 CCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1688  
 DB 601 CCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
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 DB 661 GCGCCCGAGACCGCGGAGCGCGCGCGCTGCTGACCGCGCGCTGCGCGCGCGCGCGCG 720  
 QY 1749 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1808  
 DB 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
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 DB 781 CTGTGCTCTGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
 QY 1869 CTGCGAGCGCGCGCGCTGCTGCGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1928  
 DB 841 CTGCGAGCGCGCGCGCTGCGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
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 DB 901 CGTAACTGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 QY 1989 GCGGAAACGCTGGGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2048  
 DB 961 GCGGAAACGCTGGGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 QY 2049 --TCCCTATTTGATTCGAGCTTCCAGCGCGCGGTACTTCCATCCCGGAGAAACCATG 2106  
 DB 1021 TTTCTCTATTTGATTCGAGCTTCCAGCGCGCGGTACTTCCATCCCGGAGAAACCATG 1080  
 QY 2107 TCTCTGTCCCGAGAGCTCTGCGGAGACCCGAGGCGCTTTGAGGAGTGGGATCCCGGATC 2166  
 DB 1081 TCTCTGTCCCGAGAGCTCTGCGGAGACCCGAGGCGCTTTGAGGAGTGGGATCCCGGATC 1140  
 QY 2167 CGATTTCAGTACGCGAGTGTCTTTCCAGAGCTCTGAGACCTCTGAGACCAAGAGAGAGTGTGTA 2226  
 DB 1141 CGATTTCAGTACGCGAGTGTCTTTCCAGAGCTCTGAGACCTCTGAGACCAAGAGAGAGTGTGTA 1200  
 QY 2227 TTTCTTAATCAACCACTGTTAGATGCGCAAAATGAGAGAGTCTCAAGTGTCTTTGAGA 2286  
 DB 1201 TTTCTTAATCAACCACTGTTAGATGCGCAAAATGAGAGAGTCTCAAGTGTCTTTGAGA 1260

QY 2287 AGACGAGGAGATTTTCATTAACTAAATTTTAAATTAATGTAAGTGTGAGGC 2346  
 DB 1261 AGACGAGGAGATTTTCATTAACTAAATTTTAAATTAATGTAAGTGTGAGGC 1320  
 QY 2347 TAAAGTAACTTTGCTCGTATCAAAAGTAAAGATTTGTCAGACCTGTTGTAATTTCT 2406  
 DB 1321 TAAAGTAACTTTGCTCGTATCAAAAGTAAAGATTTGTCAGACCTGTTGTAATTTCT 1380  
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 QY 2467 CCGCTTTTCAAGAAATGCTCTTCTGTTTATGTCAGGCTTGATTAACATATGGG 2526  
 DB 1441 CCGCTTTTCAAGAAATGCTCTTCTGTTTATGTCAGGCTTGATTAACATATGGG 1500  
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 QY 2587 GGGGTAGGATGCTGCTAGTAAAGTTTCTTAATTTATTTGCTGCTGCTGCTGCTGCTGCT 2646  
 DB 1561 GGGGTAGGATGCTGCTAGTAAAGTTTCTTAATTTATTTGCTGCTGCTGCTGCTGCTGCT 1620  
 QY 2647 GAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2706  
 DB 1621 GAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 QY 2707 GGTGCTGCTCTTAATGTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2766  
 DB 1681 GGTGCTGCTCTTAATGTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
 QY 2767 TTTCAAGTGGAGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2826  
 DB 1741 TTTCAAGTGGAGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
 QY 2827 CAGTACTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2886  
 DB 1801 CAGTACTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
 QY 2887 CTCTAACCTGATTTCAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2946  
 DB 1861 CTCTAACCTGATTTCAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1920  
 QY 2947 AAGTCCAGGCGAGAGGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3006  
 DB 1921 AAGTCCAGGCGAGAGGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
 QY 3007 ACTGAGAGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3066  
 DB 1981 ACTGAGAGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040

RESULT 4  
 US-10-417-820A-151  
 ; Sequence 151, Application US/10417820A  
 ; Publication No. US20030229216A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Ruoping  
 ; APPLICANT: Hsaw, Chen W.  
 ; APPLICANT: Howlitz, Kevin  
 ; APPLICANT: Chalmers, Derek T.  
 ; APPLICANT: Behan, Dominic P.  
 ; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
 ; TITLE OF INVENTION: Receptors  
 ; FILE REFERENCE: 7 US28 CON  
 ; CURRENT APPLICATION NUMBER: US/10/417, 820A  
 ; CURRENT FILING DATE: 2003-04-16  
 ; PRIOR APPLICATION NUMBER: 09/416, 760  
 ; PRIOR FILING DATE: 1999-10-12  
 ; PRIOR APPLICATION NUMBER: 09/170, 496  
 ; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: 60/110, 060



PRIOR FILING DATE: 1998-11-27  
PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,852  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/109,213  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: 60/123,944  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,945  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,948  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,951  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 151  
LENGTH: 2040  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-417-820A-151

Query Match 65.7%; Score 2013.2; DB 16; Length 2040;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2030; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 1029 ATGGGACGCCCCCTGGAGCGAGCGAGCGCCCGAGGGGGGCGGGAGCCCGCTGGGCC 1088  
DB 1 ATGGGACGCCCCCTGGAGCGAGCGAGCGCCCGAGGGGGGCGGGAGCCCGCTGGGCC 60  
QY 1089 GCGCTGCGGCTTGGCGAGCGAGCGCGCTGCTGCGCCCTTCCCTTGGGGGGGCTGATGCGG 1148  
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QY 1149 GTACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1208  
DB 121 GTACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
QY 1209 ATGCTGATGGGGGGCTACCGGGGACATGCGGACCAACCACTGTGACTGGGCGACATG 1268  
DB 181 ATGCTGATGGGGGGCTACCGGGGACATGCGGACCAACCACTGTGACTGGGCGACATG 240  
QY 1269 GCGGTGTGCGACCTACTCATCTGCTGCGGCTGCGCTGTGCACTGTACCGCTTGGCGG 1328  
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QY 1329 TCGCGGCGCTGGGTGTTCGGGGCGCTGCTGTGCGGCTGTGCTGTGCTGTGCTGTGCTGTG 1388  
DB 301 TCGCGGCGCTGGGTGTTCGGGGCGCTGCTGTGCGGCTGTGCTGTGCTGTGCTGTGCTGTG 360  
QY 1389 TGCACCTAGCGCAAGCTGTGACATGACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1448  
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DB 421 TGCAGCGCGCTGCGCGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 480  
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DB 481 GTGCTGTGGGCGGTGGGCGCTGTGCTGTGCGGCTGCTGTGCTGTGCTGTGCTGTGCTGTG 540  
QY 1569 GAGAGCCCGGAGCTTCCGTAATCCGAGGCTCAATAGCAACCGCGGAGATCCGCTTCG 1628  
DB 541 GAGAGCCCGGAGCTTCCGTAATCCGAGGCTCAATAGCAACCGCGGAGATCCGCTTCG 600  
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DB 601 CCGCTGAGCTGCGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 660  
QY 1689 GGGCGCGAGACCGCGAGGCGCGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1748

DB 661 GGGCGCGAGACCGCGAGGCGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 720  
QY 1749 CAGCTGGGCGGCGCTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1808  
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QY 1809 CTGTGCTGACATCTTCTGTACGAGGCTATCGGGGAGGAGCTGTGTGAGCAGCGCGGCGG 1868  
DB 781 CTGTGCTGACATCTTCTGTACGAGGCTATCGGGGAGGAGCTGTGTGAGCAGCGCGGCGG 840  
QY 1869 CTGCGAGGCGCGCGCGCTGCGGGCGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1928  
DB 841 CTGCGAGGCGCGCGCGCTGCGGGCGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
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DB 901 CGTAAAGTGAAGCGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 960  
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DB 961 GCGGAAAGGCTGGGTCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
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DB 1021 TTTCTTATTTGATTCAGCTTCCAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
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QY 2167 CGATTCAATACACGAGCTGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCT 2226  
DB 1141 CGATTCAATACACGAGCTGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAG 1200  
QY 2227 TTTTAAATCCAAACCACTGTGATGATGCAAAATGAGAGCTCTCAAGCTCTTGA 2286  
DB 1201 TTTTAAATCCAAACCACTGTGATGATGCAAAATGAGAGCTCTTGA 1260  
QY 2287 AGAGAGGGAGATTTCACTTAAGCTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2346  
DB 1281 AGAGAGGGAGATTTCACTTAAGCTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1320  
QY 2347 TAAAGTAAACCTTGTCTGTATCAAAAGTAAAGTGTGAGACCTGTGTAGATTTCT 2406  
DB 1321 TAAAGTAAACCTTGTCTGTATCAAAAGTAAAGTGTGAGACCTGTGTAGATTTCT 1380  
QY 2407 TTCAACAGAGAAAGAAACTTGTCTCGAAGTGGTGTGTGAAGAAAGCTGCGCAAGG 2466  
DB 1381 TTCAACAGAGAAAGAAACTTGTCTCGAAGTGGTGTGTGAAGAAAGCTGCGCAAGG 1440  
QY 2467 CGGCTGTGTGAGAAATGCTCTCTGTGATGATGCAAGCTGATGATGATGATGATGATGATGATGAT 2526  
DB 1441 CGGCTGTGTGAGAAATGCTCTCTGTGATGATGCAAGCTGATGATGATGATGATGATGATGATGAT 1500  
QY 2527 AGCTTACTAGCAATTTTAAAGCAAGTATCATGACAGCTGACAGCTGTGATTTTCT 2586  
DB 1501 AGCTTACTAGCAATTTTAAAGCAAGTATCATGACAGCTGACAGCTGTGATTTTCT 1560  
QY 2587 GGGGTGAGGATCTGCTAGGATGAGATTTCTGATTTATTTATTTATTTATTTATTTATTTATTTAT 2646  
DB 1561 GGGGTGAGGATCTGCTAGGATGAGATTTCTGATTTATTTATTTATTTATTTATTTATTTATTTAT 1620  
QY 2647 GCAGATGATCTTGTGCGGGTGGGGGTTTATTTGCTTCCAGTCTTTTGTAAATCC 2706  
DB 1621 GCAGATGATCTTGTGCGGGTGGGGGTTTATTTGCTTCCAGTCTTTTGTAAATCC 1680  
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DB 1681 GGTGCTGTGCTGTATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1740  
QY 2767 TTCCAGCTGTGAGAAATCATTTATCAATAAACGAGATTCGCGAGTGTGATTTCTCT 2826

Db 1741 TTCACGTTGGAGATTCATTACATAAACAAGAGATTGGGATGATGATCTTCT 1800  
QY 2827 CAGTACTTAAACATGCTGCTTGAACCTTTTCTATCTGAGCGCATCTATCAACCAATC 2886  
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QY 2887 CTCTACAACTCATTTTCAAAAGATGACAGAGCGGCGCTTAAAGCTGCTGCAAGG 2946  
Db 1861 CTCTACAACTCATTTTCAAAAGATGACAGAGCGGCGCTTAAAGCTGCTGCAAGG 1920  
QY 2947 AAGTCCAGCCGAGAGCGCTTCCAGAGAGCAAGCACTGGCGGGAATTGCAAGGAC 3006  
Db 1921 AAGTCCAGCCGAGAGCGCTTCCAGAGAGCAAGCACTGGCGGGAATTGCAAGGAC 1980  
QY 3007 ACTGAGAGAGACACGCTGGGCTTACCCGAGACAGCGCTAACCTGGAAGAGATGGGATA 3066  
Db 1981 ACTGAGAGAGACACGCTGGGCTTACCCGAGACAGCGCTAACCTGGAAGAGATGGGATA 2940

RESULT 5  
US-10-225-567A-472  
; Sequence 472, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 472  
; LENGTH: 1239  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-225-567A-472

Query Match 29.4%; Score 901; DB 15; Length 1239;  
Best Local Similarity 100.0%; Pred. No. 8.2e-207;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1029 ATGGGACAGCCCTTGAGAGCGAGCGAGCGGCGGAGCGGCGGAGCGCGTGGCC 1088  
Db 1 ATGGGACAGCCCTTGAGAGCGAGCGAGCGGCGGCGGAGCGGCGGAGCGCGCTGGCC 60  
QY 1089 GCGCTGCGCGCTTGGAGAGCGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGATCCG 1148  
Db 61 GCGCTGCGCGCTTGGAGAGCGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGATCCG 120  
QY 1149 GTGACCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208  
Db 121 GTGACCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
QY 1209 ATGTGATCGGCGCTTACCGGAGATGCGGACCAACCACTTGTACTTGGGAGAGATG 1268  
Db 181 ATGTGATCGGCGCTTACCGGAGATGCGGACCAACCACTTGTACTTGGGAGAGATG 240  
QY 1269 GCGCTGCTCGACCTTACTATCTGCTGCGGCTGCGGCTTGAACCTGTACCGCTCTGCGC 1328  
Db 241 GCGCTGCTCGACCTTACTATCTGCTGCGGCTGCGGCTTGAACCTGTACCGCTCTGCGC 300  
QY 1329 TCGCGCCCTGGGTGCTTGGGCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1388  
Db 301 TCGCGCCCTGGGTGCTTGGGCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 360  
QY 1389 TGCACCTTACGCGCTGCTGCAATGACCGGCGCTACGCGTGTAGAGCGCTTACTGGCATC 1448  
Db 361 TGCACCTTACGCGCTGCTGCAATGACCGGCGCTACGCGTGTAGAGCGCTTACTGGCATC 420

QY 1449 TGCACCGCGCTTCCGCGCCCGCGCTCTTGTACACCCCGCGCGGCTCCGCGCGCTCATCGCT 1508  
Db 421 TGCACCGCGCTTCCGCGCCCGCGCTCTTGTACACCCCGCGCGGCTCCGCGCGCTCATCGCT 480  
QY 1509 GTGACTGTGGGCGGTGAGCGCTGCTCTGCGCGGCTTCTTGTCTGAGTGGGCGTCCAG 1568  
Db 481 GTGACTGTGGGCGGTGAGCGCTGCTCTGCGCGGCTTCTTGTCTGAGTGGGCGTCCAG 540  
QY 1569 CAGGACCCCGGCAATCTCCGTAATCCCGGCGCTCAATGCAACCGCGGATCCCTCTCCG 1628  
Db 541 CAGGACCCCGGCAATCTCCGTAATCCCGGCGCTCAATGCAACCGCGGATCCCTCTCCG 600  
QY 1629 CCTCTGCGCTGCTGCGCGCTCTCTGAGCTGCTGCGCGGCGCAACCGCGCGCGCGCTGCG 1688  
Db 601 CCTCTGCGCTGCTGCGCGCTCTCTGAGCTGCTGCGCGGCGCAACCGCGCGCGCTGCG 660  
QY 1689 GGGCCCGAGACCGCGGAGCGCGCGCGCTGTTCAAGCCGGAATGCGCGCGAGCCCGCG 1748  
Db 661 GGGCCCGAGACCGCGGAGCGCGCGCGCTGTTCAAGCCGGAATGCGCGCGAGCCCGCG 720  
QY 1749 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1808  
Db 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 1809 CTGTGCTCAGCATCTCTACGAGGCTCATCGGCGGAGCTGTGAGACAGCGCGCGCG 1868  
Db 781 CTGTGCTCAGCATCTCTACGAGGCTCATCGGCGGAGCTGTGAGACAGCGCGCGCG 840  
QY 1869 CTGTGAGCGCGCGCGCGCTGCGGCGGAGAGAGCGCACCGGACAGCGCTGCGCTCTG 1928  
Db 841 CTGTGAGCGCGCGCGCGCTGCGGCGGAGAGAGCGCACCGGACAGCGCTGCGCTCTG 900  
QY 1929 C 1929  
Db 901 C 901

RESULT 6  
US-10-290-078-13  
; Sequence 13, Application US/10290078  
; Publication No. US20030124596A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph A.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; FILE REFERENCE: MP12001-288P1(M)  
; CURRENT APPLICATION NUMBER: US/10/290,078  
; CURRENT FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 1239  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-290-078-13

Query Match 29.4%; Score 901; DB 15; Length 1239;  
Best Local Similarity 100.0%; Pred. No. 8.2e-207;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1029 ATGGGACAGCCCTTGAGAGCGAGCGAGCGGCGGAGCGGCGGAGCGCGCTGGCC 1088  
Db 1 ATGGGACAGCCCTTGAGAGCGAGCGAGCGGCGGAGCGGCGGAGCGCGCTGGCC 60  
QY 1089 GCGCTGCGCGCTTGGAGAGCGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGATCCG 1148  
Db 61 GCGCTGCGCGCTTGGAGAGCGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGATCCG 120  
QY 1149 GTGACCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208  
Db 121 GTGACCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180





Db 249 TCCCCCTGACCTCTTCCGCTCTGGGAGTACCGGCTTTGAACTTGGACCTGCTCT 308  
Qy 1360 GCCGCTGTCCCTCTACGTGGGCGAGGGCTGACCTTACCGCAGCTGCTGCATGACCG 1419  
Db 309 GCAACTCTTCCAGTGTGTTAGCGAGCTGACCTTACCGCAGAGTCTCACCATACCG 368  
Qy 1420 CGCTCAGGTGAGGAGCTTACCTGGCCATCTGCGCCCGCTCCGCGCCGCTTGTGTC 1479  
Db 369 CGCTGAGGTGAGGAGCTTACCTGGCCATCTGCGCCCGCTCCGCGCCGCTTGTGTC 428  
Qy 1480 CCGGCGCGCGCTCCGCGCGCTTACCTGCTGCTGCTGGGCGCTGCGCTGCTGCTGCG 1539  
Db 429 CCAAGGGCGCGGTAAAGTGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 488  
Qy 1540 GTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1581  
Db 489 GGGCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530

RESULT 10  
US-10-303-204A-4  
; Sequence 4, Application US/10303204A  
; Publication No. US2003016514A1  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris P.  
; APPLICANT: Feighner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, Paul A.  
; APPLICANT: Schaeffer, James M.  
; APPLICANT: Van Der Ploeg, Leonardus H. T.  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR  
; FILE REFERENCE: 19589PCA  
; CURRENT APPLICATION NUMBER: US/10/303,204A  
; CURRENT FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 09/077,674  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: PCT/US96/19445  
; PRIOR FILING DATE: 1996-12-10  
; PRIOR APPLICATION NUMBER: 60/018,962  
; PRIOR FILING DATE: 1996-06-06  
; PRIOR APPLICATION NUMBER: 60/008,582  
; PRIOR FILING DATE: 1995-12-13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 4  
; LENGTH: 1029  
; TYPE: DNA  
; ORGANISM: sus scrofa  
US-10-303-204A-4

Query Match 7.5%; Score 230; DB 15; Length 1029;  
Best Local Similarity 68.6%; Pred. No. 4.2e-45;  
Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;  
Qy 1120 CGCCTTTCCTTCCGCGCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1179  
Db 266 CGCCTTTCCTTCCGCGCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325  
Qy 1180 TCGGGGTGAGCGGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1239  
Db 326 TGGGTATCGCGGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 385  
Qy 1240 CCAACCAACTTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1299  
Db 386 CCAACCAACTTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445  
Qy 1300 TGGCGTTCGACCTGTAACCGCTGCTGCGGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTG 1359  
Db 446 TGGCGTTCGACCTTTCGCGCTTTCGCGGCTGCGGCGCTTGGAACTTGGCAACTGCTCT 505

Qy 1360 GCCGCTGTCCCTCTACGTGGGCGAGGGCTGACCTTACCGCAGCTGCTGCATGACCG 1419  
Db 506 GCAACTCTTCCAGTGTGTTAGCGAGCTGACCTTACCGCAGAGTCTCACCATACCG 565  
Qy 1420 CGCTCAGGTGAGGAGCTTACCTGGCCATCTGCGCCCGCTCCGCGCCGCTTGTGTC 1479  
Db 566 CGCTGAGGTGAGGAGCTTACCTGGCCATCTGCGCCCGCTCCGCGCCGCTTGTGTC 625  
Qy 1480 CCGGCGCGCGCTCCGCGCGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1539  
Db 626 CCAAGGGCGCGGTAAAGTGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 685  
Qy 1540 GTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1581  
Db 686 GGGCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727

RESULT 11  
US-10-305-720-359  
; Sequence 359, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Yang, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
; SOFTWARE: PERL Program  
; SEQ ID NO: 359  
; LENGTH: 250  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20040010136A1 2018536  
; NAME/KEY: unsure  
; LOCATION: (1) ... (250)  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-305-720-359

Query Match 7.5%; Score 229; DB 16; Length 250;  
Best Local Similarity 98.8%; Pred. No. 4.3e-45;  
Matches 240; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
Qy 2824 TCTCAGTACTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2883  
Db 1 TCTCAGTACTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60  
Qy 2884 ATCTCTTCAACCTTCAATTTCAAGAGTACAGAGCGGCGCTTTAACTGCTGCTGCTGCA 2943  
Db 61 ATCTCTTCAACCTTCAATTTCAAGAGTACAGAGCGGCGCTTTAACTGCTGCTGCTGCA 120  
Qy 2944 AGAAGTTCAGAGCGGAGAGGCTTTCACAGAGAGGAGCACTGCGGGGAAAGTTGCGAGG 3003  
Db 121 AGAAGTTCAGAGCGGAGAGG-TTCCACAGAGAGGAGCACTGCGGGGAAAGTTGCGAGG 179  
Qy 3004 GACACTGAGAGAGCAAGTGGGCTACACCGAGAGCAAGCCCTAACTGAGAGAGAGTGGGA 3063  
Db 180 GACACTGAGAGAGCAAGTGGGCTACACCGAGAGCAAGCCCTAACTGAGAGAGATGGGA 239  
Qy 3064 TAA 3066  
Db 240 TAA 242

RESULT 12  
US-10-225-567A-139  
; Sequence 139, Application US/10225567A  
; Publication No. US20030113798A1



Db 840 CGAATGCGCGCCCAACGATTGCGGTGCGTGAATCTCAACGGTCAATGCTGAGG 899  
Qy 1660 CGCGGGGCGCCACCGCGCGCCCGCGTGGGGGCGCCGAGACCGGAGAGCGCGCGCTGT 1719  
Db 900 GTCCAGGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 959  
Qy 1720 TCAGCCCGGAATGCGCGCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1779  
Db 960 CAGGAAGCTGTGTGGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1019  
Qy 1780 TCACCAACGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1839  
Db 1020 GACCAACAGCAACCGTGAATGCTGGTGGTCTCAAGCGCGCGCGCGCGCGCGCG 1079  
Qy 1840 GCGCGGAGCTGT 1851  
Db 1080 CGCGGCTCTAT 1091

RESULT 14  
US-10-303-204A-15  
; Sequence 15, Application US/10303204A  
; Publication No. US2003016614A1  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris F.  
; APPLICANT: Feighner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, James M.  
; APPLICANT: Schaeffer, Paul A.  
; APPLICANT: Van Der Ploeg, Leonardus H. T.  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR  
; TITLE OF INVENTION: FAMILY  
; FILE REFERENCE: 19589PCA  
; CURRENT APPLICATION NUMBER: US/10/303, 204A  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: PCT/US96/19445  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: PCT/US96/19445  
; PRIOR FILING DATE: 1996-12-10  
; PRIOR APPLICATION NUMBER: 60/018,962  
; PRIOR FILING DATE: 1996-06-06  
; PRIOR APPLICATION NUMBER: 60/008,582  
; PRIOR FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 1092  
; TYPE: DNA  
; ORGANISM: rattus norvegicus  
US-10-303-204A-15

Query Match 7.4%; Score 228.4; DB 15; Length 1092;  
Best Local Similarity 68.4%; Pred. No. 1.1e-44;  
Matches 316; Conservative 0; Mismatches 146; Indels 0; Gaps 0;  
Qy 1120 CGCCCTTCCCTGGGGGCGCTGTGCGGTGACCGCTGTGCTGCTGTGCTGTGCTG 1179  
Db 104 CGCTGTCCCGCTCGCTGCTGCGAGGCTGACCGGCACTGCGTGGGCGCTTGTGG 163  
Qy 1180 TCGGGGTGAGCGGCAAGTGTGACCGTGTGCTGTATCGGGCGCTACCGGAGATCGGA 1239  
Db 164 TGGGCACTCTGAGGAACCTGTCTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 223  
Qy 1240 CCACCAACCACTTGTACTGTGAGGAGATGAGCGCTGTCCGACTACTATCTGTGCGGC 1299  
Db 224 CCACCAACCACTTGTACTGTGAGGAGATGAGCGCTTTCGATCTGTCTTCTGTGA 283  
Qy 1300 TCGCGTTGACCTGTACCGCTTGTGGGCTGCGGCGCTGGGTGTGGGCGCGCTGTCT 1359  
Db 284 TCGCGGTGACCTGTGTCCGCTCTGCGAGTACCGGCGCTGGAACCTTGTGGGCGAGCTGTCT 343

Qy 1360 GCGCGCTTCCCTCTACGTGGGCGAGGAGCTGACCTTACGCCAGCTGTCTGACATGACCG 1419  
Db 344 GCAAACTTTCAGATTGTTCAGCGAGAGCTGACACTTACGCCACCGTCTTCACTATCACCG 403  
Qy 1420 CGCTCAGGTGAGCGCTACTGTGCGCATCTGCGCGCGCGCTCGCGCGCGCGCTGTGTGCA 1479  
Db 404 CGCTGAGGTGAGCGCTACTGTGCGCATCTGCGCGCGCGCTCGCGCGCGCGCTGTGTGCA 463  
Qy 1480 CCGCGCGCGCGCTCGCGCGCTGCTGCTGTGCTGTGCGCGCGCGCTGTGCGCGCG 1539  
Db 464 CTAAAGGCGCGGTGAAGCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 523  
Qy 1540 GTCCCTTGTGTCTGT 1581  
Db 524 GCGCATCTTGT 565

RESULT 15  
US-10-303-204A-14  
; Sequence 14, Application US/10303204A  
; Publication No. US2003016614A1  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris F.  
; APPLICANT: Feighner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, James M.  
; APPLICANT: Schaeffer, Paul A.  
; APPLICANT: Van Der Ploeg, Leonardus H. T.  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR  
; TITLE OF INVENTION: FAMILY  
; FILE REFERENCE: 19589PCA  
; CURRENT APPLICATION NUMBER: US/10/303, 204A  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 09/077,674  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: PCT/US96/19445  
; PRIOR FILING DATE: 1996-12-10  
; PRIOR APPLICATION NUMBER: 60/018,962  
; PRIOR FILING DATE: 1996-06-06  
; PRIOR APPLICATION NUMBER: 60/008,582  
; PRIOR FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 3129  
; TYPE: DNA  
; ORGANISM: rattus norvegicus  
US-10-303-204A-14

Query Match 7.4%; Score 228.4; DB 15; Length 3129;  
Best Local Similarity 68.4%; Pred. No. 1.1e-44;  
Matches 316; Conservative 0; Mismatches 146; Indels 0; Gaps 0;  
Qy 1120 CGCCCTTCCCTGGGGGCGCTGTGCGGTGACCGCTGTGCTGCTGTGCTGTGCTG 1179  
Db 104 CGCTGTCCCGCTCGCTGCTGCGAGGCTGACCGGCACTGCGTGGGCGCTTGTGG 163  
Qy 1180 TCGGGGTGAGCGGCAAGTGTGACCGTGTGCTGTATCGGGCGCTACCGGAGATCGGA 1239  
Db 164 TGGGCACTCTGAGGAACCTGTCTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 223  
Qy 1240 CCACCAACCACTTGTACTGTGAGGAGATGAGCGCTGTCCGACTACTATCTGTGCGGC 1299  
Db 224 CCACCAACCACTTGTACTGTGAGGAGATGAGCGCTTTCGATCTGTCTTCTGTGA 283  
Qy 1300 TCGCGTTGACCTGTACCGCTTGTGGGCTGCGGCGCTGGGTGTGGGCGCGCTGTCT 1359  
Db 284 TCGCGGTGACCTGTGTCCGCTCTGCGAGTACCGGCGCTGGAACCTTGTGGGCGAGCTGTCT 343  
Qy 1360 GCGCGCTTCCCTCTACGTGGGCGAGGAGCTGACCTTACGCCAGCTGTCTGACATGACCG 1419  
Db 344 GCAAACTTTCAGATTGTTCAGCGAGAGCTGACACTTACGCCACCGTCTTCACTATCACCG 403



QY 1420 CGCTCAGCGTCGAGCGGCTACCTGAGCCATCTGCCGCCCGCTCCGCGCCCGGCTCTTGATCA 1479  
 Db 404 CGCTGAGCGTCGAGCGGCTACCTGAGCCATCTGCCGCCCGCTCCGCGCCCGGCTCTTGATCA 463  
 QY 1480 CCCGCGCGCGGTCGCCGCTCATCGCTGCTTGAGCCGATGCGCGCTGCTCTGCGG 1539  
 Db 464 CTAGGCGCGGTCGAGCGGCTCATCTGTCATCTGCGCGCTGCTCTGCGAGCGCG 523  
 QY 1540 GTCCCTTCTTGTCTGCTGAGCGCTGAGCAGAGACCCCGCA 1581  
 Db 524 GCGCCATCTTCTGCTGAGCGCTGAGCAGAGACCCCGCA 565

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 Job time : 1295 secs

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Thu Jul 22 08:37:31 2004

us-09-719-485-1.rst

Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 16:22:38 ; Search time 7448 Seconds

(without alignments)  
12292.890 Million cell updates/sec

Title: US-09-719-485-1

Perfect score: 3066

Sequence: 1 ttgaattatctgctcctcgtg.....acgtgaagacgatgggataa 3066

Scoring table: IDENTITY\_NUC

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estrov:\*  
6: em\_estrpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_esthum:\*  
16: em\_estom:\*  
17: em\_ges\_hum:\*  
18: em\_ges\_huv:\*  
19: em\_ges\_pln:\*  
20: em\_ges\_vrl:\*  
21: em\_ges\_fun:\*  
22: em\_ges\_mam:\*  
23: em\_ges\_mus:\*  
24: em\_ges\_pro:\*  
25: em\_ges\_rtd:\*  
26: em\_ges\_phg:\*  
27: em\_ges\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	693.8	22.6	843	13	BUS53576
2	576	18.8	580	10	BFS13101
3	490.2	16.0	495	10	BFS12085
4	360.6	11.8	399	28	AQ939773

5	255.8	8.3	425	28	AQ138681	HS_3073_A
6	231.6	7.6	1046	29	AY407666	Mus muscu
7	230	7.5	4435	11	AK049671	Mus muscu
8	227.8	7.4	1052	29	AY407664	Homo sapi
9	226.8	7.4	500	10	BF603623	269181 MA
10	219.2	7.1	608	13	BY724644	BY724644
11	213.2	7.0	969	29	AY407665	Pan trogl
12	204	6.7	370	13	EX485214	AY407665
13	200.8	6.5	489	9	AL042230	DKFZP686
14	198.2	6.5	2669	11	BC035179	BC035179
15	197.8	6.5	606	13	BQ778458	Homo sapi
16	197.8	6.5	619	13	EX505458	DKFZP686
17	197.8	6.5	712	14	CD246087	CD246087
18	197.8	6.5	721	14	CD364665	UT-H-FR2
19	197.8	6.5	729	14	CA442904	UT-H-DP0
20	197.2	6.4	982	13	EX370686	EX370686
21	196.8	6.4	639	12	BM992802	UI-H-DT0
22	196.2	6.4	391	9	AI569401	AI569401
23	196.2	6.4	656	14	CA420015	CA420015
24	196	6.4	741	29	AG113248	Par trogl
25	195.2	6.4	337	13	BUS66880	AGENCOURT
26	194.8	6.4	457	10	BF939646	BF939646
27	193.6	6.3	416	14	CD520893	CD520893
28	193.4	6.3	353	9	AV657198	AV657198
29	193.4	6.3	854	28	AQ747659	AQ747659
30	193	6.3	537	28	AQ122719	HS_5533_A
31	193	6.3	739	28	AQ35003	AG0322719
32	192.6	6.3	486	12	BG231842	CIT-HSP-2
33	192.6	6.3	624	14	CA423118	CA423118
34	192.6	6.3	691	14	CD243422	CD243422
35	192.6	6.3	953	12	BI084622	AGENCOURT
36	192.4	6.3	680	12	BM990843	BI084622
37	192.2	6.3	623	9	AV703573	UI-H-DI0
38	192	6.3	546	9	AI889995	BM990843
39	192	6.3	699	28	AQ389756	AV703573
40	191.4	6.2	365	14	CD688147	wm80c03.x
41	191.4	6.2	447	13	EX489032	AQ389756
42	191.2	6.2	2546	11	BC027960	RPCL11-15
43	191	6.2	538	9	AU143917	CD688147
44	191	6.2	556	13	BQ183587	ES14669 H
45	191	6.2				ES14669 H

## ALIGNMENTS

RESULT 1  
BUS53576 843 bp mRNA linear EST 16-SEP-2002  
LOCUS  
DEFINITION AGENCOURT 10242213 NIH MGC 109 Homo sapiens CDNA clone  
IMAGE:6577973 5', mRNA sequence.  
ACCESSION BUS53576  
VERSION BUS53576.1 GI:229303848  
KEYWORDS  
SOURCE  
ORGANISM  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
NIH-MGC <http://mgc.ncl.nih.gov/>  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strauberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LNCM278 row: P column: 05  
High quality sequence stop: 534.

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		/db_xref="taxon:9606"	
		/clone="IMAGE:6577973"	
		/tissue_type="teratocarcinoma, cell line"	
		/lab_host="DH10B (phage-resistant)"	
		/clone_lib="NIH_MGC_109"	
		/note="Organ: ovary; Vector: pOT87; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
ORIGIN			
Query Match		22.6%; Score 693.8; DB 13; Length 843;	
Best Local Similarity		96.6%; Pred. No. 1.6e-73;	
Matches 773; Conservative		0; Mismatches 18; Indels 9; Gaps 6;	
QY	2202	TTGAGCCGAAAGAGAGTTGGTAACTTTTATTCACACCACTCTTGTGATGCCAATAATG	2261
DB	1	TTGAGCCGAAAGAGAGTTGGTAACTTTTATTCACACCACTCTTGTGATGCCAATAATG	60
QY	2262	AGGAGTCTCAAGTGTCTTGAGAGACGAGAGATTTCATTAGCTAAATTTT	2321
DB	61	AGGAGTCTCAAGTGTCTTGAGAGACGAGAGATTTCATTAGCTAAATTTT	120
QY	2332	TTTATGTATGATGATGCTGAAGGCTTAAGTAACTTGTCTGATCAAAAGTAAAGAT	2381
DB	121	TTTATGTATGATGATGCTGAAGGCTTAAGTAACTTGTCTGATCAAAAGTAAAGAT	180
QY	2382	TGTGACAGACCTGTTGTGAATTTCTTTCACAGAGAACAGAAACTGTCTCGAAGTGG	2441
DB	181	TGTGACAGACCTGTTGTGAATTTCTTTCACAGAGAACAGAAACTGTCTCGAAGTGG	240
QY	2442	GTTTGTGAAAGAGAGCTTGCAGAGCGCTTGTTCAGAGAAATGCTCTTCTGTTTAT	2501
DB	241	GTTTGTGAAAGAGAGCTTGCAGAGCGCTTGTTCAGAGAAATGCTCTTCTGTTTAT	300
QY	2502	GTCAGAGCTTGATACACATATGGGAGCTTACATGATGATTTAAGCAAGTATTCATGC	2561
DB	301	GTCAGAGCTTGATACACATATGGGAGCTTACATGATGATTTAAGCAAGTATTCATGC	360
QY	2562	AGCCTGAGCCTGATCAATTTTCTGGGATGAGATCTGCTAGTAGAAGTTTCTCTA	2621
DB	361	AGCCTGAGCCTGATCAATTTTCTGGGATGAGATCTGCTAGTAGAAGTTTCTCTA	420
QY	2622	ATTATTTTGTCTTACTTGTATATGACATGTTCTCTTGTGGGGTGGGGGTTTATTT	2681
DB	421	ATTATTTTGTCTTACTTGTATATGACATGTTCTCTTGTGGGGTGGGGGTTTATTT	480
QY	2682	GCTTCCCATGCTTTTGTATATCCGGTGTGTCTTATGTT-GCAGTGGT-GGTGGTT	2739
DB	481	GCTTCCCATGCTTTTGTATATCCGGTGTGTCTTATGTT-GCAGTGGT-GGTGGTT	540
QY	2740	CTTGAGATTTTATTTTGTCTGTTGCTTCCATCGATGGAGATCATTTTCAATAACG	2799
DB	541	CTTGAGATTTTATTTTGTCTGTTGCTTCCATCGATGGAGATCATTTTCAATAACG	600
QY	2800	GAAGATTCGGAGATGATGATCTCTCTAGTACTTAAATCATGCTGCTGCACTTTTC	2859
DB	601	GAAGATTCGGAGATGATGATCTCTCTAGTACTTAAATCATGCTGCTGCACTTTTC	660
QY	2860	TATCTGAGGAGATCTATCAACCAATCTCTCAACCTG-ATTCAAGAAAGTAC-AGAG	2917
DB	661	TATCTGAGGAGATCTATCAACCAATCTCTCAACCTG-ATTCAAGAAAGTAC-AGAG	720
QY	2918	CGGCGGCTTTTAA-----CTGGTGTCTCGAAGAAAGTCCAGGCCGAG-AGGCTTCAAG	2972

DB 721 CGGCGGCTTTTAACTGCTGCTTCCGAGGAAGTCCAGGCCAGAGAGCTCCACAG 780

QY 2973 AAGCAGGACACTGCGGGG 2992

DB 781 AAGCAGGACACTGCGGGG 800

RESULT 2

BF513101

LOCUS

DEFINITION

UI-H-BM1-ann-e-07-0-UI-s1 NCI CGAP\_Sub7 Homo sapiens cDNA clone

IMAGE:3070549 3', mRNA sequence.

BF513101

ACCESSION

BF513101.1 GI:11598280

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 590)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

Oligo-dT track not found, Not 1 site shown in beginning of sequence is likely internal to the message. cDNA library preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution

Information can be found through the I.M.A.G.E. Consortium/ILMIL at: [www.bio.lmli.gov/bbrp/image/image.html](http://www.bio.lmli.gov/bbrp/image/image.html)

Seq primer: M13 Forward

POLYA=No.

FEATURES

source

1. 590

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3070549"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP Sub7"

/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Sca RI; NCI CGAP Sub7 is a subcloned library derived from NCI CGAP Sub6. The NCI CGAP Sub7 library had 12 million recombinants. A single-stranded DNA preparation of NCI CGAP Sub6 was used as a tracer in a subtractive hybridization with a driver comprising the IMAGE pool (NCI CGAP Kid3 pool 1 LLM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids 132376-132391, 1456008-1456775, 1500552-1502855); NCI CGAP Kid5 pool 1 LLM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI CGAP LMS pool 1 LLM 3575-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1524339); NCI CGAP GC4 pool 1 LLM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI CGAP pr22 pool 1 LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP C010 pool 1 LLM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144564-1145351). (% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub2 (IMAGE Clonoids 270816-2710535) and NCI CGAP Sub2 (IMAGE Clonoids 2710536-2714555) (4% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clonoids 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE Clonoids 2723592-2729326) (40% of the driver population), plus a pool of 4032 clones from NCI CGAP Sub5 (IMAGE Clonoids 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described (Bonaldi, Lennon & Soares (1996):



QY 822 GGGGAGAGAGCTGGGAGAGCTGGGAGAGCGCTTGGAGAGCCAGCCCGAGAGCGCT 881  
 Db 195 GGGGAGAGAGCTGGGAGAGCTGGGAGAGCGCTTGGAGAGCCAGCCCGAGAGCGCT 136  
 QY 882 TCTGCGCGCGCGAGAGAGCGAGCGAGCGCTTGGAGAGCGCTTGGAGAGCGCGAGAGCGT 941  
 Db 135 TCTGCGCGCGCGAGAGAGCGAGCGAGCGCTTGGAGAGCGCGAGAGCGCGAGAGCGT 76  
 QY 942 CGGCTGGGAGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGT 1001  
 Db 75 CGGCTGGGAGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGT 16  
 QY 1002 GGGAGCGGCGGCGCGCG 1016  
 Db 15 GGGAGCGGCGGCGCGCG 1

RESULT 4  
 LOCUS A039773/c 399 bp DNA linear GSS 23-AUG-2000  
 DEFINITION N55-116R Human NotI clones Homo sapiens genomic, genomic survey  
 ACCESSION A039773  
 VERSION A039773.1 GI:7216151  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 399)  
 Zabarovsky, E.R., Gzatalullin, R., Podowski, R.M., Zabarovsky, V.V., Li, J., Muravenko, O.V., Kozhev, S., Petrenko, L., Skobelev, N., Li, J., Protodopov, A., Kashuba, V., Ernborg, I., Winberg, G. and Wahlstedt, C.  
 NotI clones in the analysis of the human genome  
 Nucleic Acids Res. 28 (7), 1635-1639 (2000)

TITLE  
 JOURNAL MEDLINE  
 PUBMED 10710430  
 COMMENT Contact: Podowski RM  
 Center for Genomics Research  
 Karolinska Institute  
 17177 Stockholm, Sweden  
 Tel: +46-8-728-6372  
 Fax: +46-8-337983  
 Email: Raf.Podowski@cgr.ki.se  
 Class: NotI site.  
 Location/Qualifiers  
 1..399  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
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FEATURES  
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 Matches 380; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

Db 215 CGGGGAGAGCGCGCGCGCTGGGAGAGCTGGGAGAGCGCTTGGAGAGCCAGCCCGAGAGCGCT 156  
 QY 863 CCACACCCGAGAGAGCGCTTGGAGAGCGCGCGAGAGCGAGCGAGCGAGCGAGCGAGCGT 922  
 Db 155 CCACACCCGAGAGAGCGCTTGGAGAGCGCGCGAGAGCGAGCGAGCGAGCGAGCGAGCGT 96  
 QY 923 CTGGCGCGCGCGAGAGCGCGCTGGGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGT 982  
 Db 95 CTGGCGCGCGCGAGAGCGCGCTGGGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGT 36  
 QY 983 CAGGCTCCAGAGCGAGCGCGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGT 1017  
 Db 35 CAGGCTCCAGAGCGAGCGCGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGT 1

RESULT 5  
 LOCUS A0138681 425 bp DNA linear GSS 24-SEP-1998  
 DEFINITION HS 3073 A2 D02 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=4 Row=G, genomic survey  
 ACCESSION A0138681  
 VERSION A0138681.1 GI:3529334  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 425)  
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.  
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 99380589  
 10449764

TITLE  
 JOURNAL MEDLINE  
 PUBMED 10449764  
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Sequence Tagged Connector  
 Plate: 3073 row: G column: 4  
 Class: BAC ends  
 High quality sequence stop: 425.  
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FEATURES  
 source

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 Best Local Similarity 94.2%; Pred. No. 3.2e-21;  
 Matches 274; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Db 171 CACATATGGAGGACCTACTACTAGTTTAAAGCAAGTATCCATCAGCTGGACCTGGT 230  
 QY 2577 CATTTTTCGTGGGGTGAAGATCTGCCTAGTAGAAGTTTCTCTAATTAATTTTGTGT 2636  
 Db 231 CATTTTTCGTGGGGTGAAGATCTGCCTAGTAGAAGTTTCTCTAATTAATTTGTGTG-T 289  
 QY 2637 ACTGTTTTCGACATGGTTCTCTGTGGGGGTGGGGGGTTATTTGCTTC 2687  
 Db 290 ACTGTATAGCAAGATGGTTCTTGTGGGTGGAGGGTTATTTGCTTCCC 340

RESULT 6  
 AY407666 1046 bp DNA linear GSS 15-DEC-2003  
 LOCUS Mus musculus GH5F gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION AY407666  
 VERSION AY407666.1 GI:39763637  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1046)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeleo,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,D.J.,  
 Adams,M.D. and Cargill,M.  
 Interfering nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeleo,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,D.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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 /gene="GH5F"  
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 Best Local Similarity 68.8%; Pred. No. 1.8e-18;  
 Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 1120 CGCCCTTCCCTGCGGGCGCTGTGCGGCTGACCGCTGTGTGCTGTGCTGTGCTG 1179  
 Db 55 CACTGTTCGCCCGCGCGCTGTGCGGGCGCTCACTGCACACTGTGCTGCGCTGTGCTG 114  
 QY 1180 TCGGGGTGAGCGGGAACCTGTGTACCGTGAATGCTGAATCGGGCGCTTACCGGACATGGGA 1239  
 Db 115 TGGGCATCTCGGGGAACCTGTGTACCGTGAATGCTGAATGCTGTGCGGAGCTGGCA 174  
 QY 1240 CCACCAACCACTTGTACCTGGGAGCAGTGGCCGTGTCCGACTTACTGCTCTGCTCGGGC 1299  
 Db 175 CCACCAACCACTTGTACCTGGGAGCAGTGGCCGTGTCCGACTTACTGCTCTGCTGGCA 234  
 QY 1300 TGGCGTTGACCTGTACCGCTCTGGGCGCTTGGCGGCGCTTGGGCTGTGCTGCTCT 1359  
 Db 235 TGGCGTTGACCTGTACCGCTCTGGGCGCTTGGCGGCGCTTGGGCTGTGCTGCTCT 294

QY 1360 GCCGCTGTCCCTCTTACGTGGGCGAGGGCTGCACCTTACGCCACGCTGCTGCATGACCG 1419  
 Db 295 GCMAACTCTTCCAGATTTGTTCAGCGAGCTGCACCTTACGCCACGCTGCTGCATGACCG 354  
 QY 1420 CGGTAGCGGTGAGAGGCTACCTGTCATCTGCGCGCGCGCTCGCGCGCGCGCTTGTGCTGA 1479  
 Db 355 CGGTAGCGGTGAGAGGCTACCTGTCATCTGCGCGCGCGCTCGCGCGCGCGCTTGTGCTGA 414  
 QY 1480 CCGGCGCGCGCGCTGCGCGCGCTCATGCTGTGCTGCTGCGCGCGCTGCTGCTGCGCG 1539  
 Db 415 CCAGAGCGCGGTGGAAGCTGTATCTGCTCATCTGCGCGCGCTGCGCGCGCTGCTGCGCG 474  
 QY 1540 GTCCCTTCTTGTTCCTGTGGTGGCGCTGCAGCGACGACCCCGCA 1581  
 Db 475 GGCCCATCTTCTGTGCTGTGGCGCTGCAGCGACGACCGCA 516

RESULT 7  
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 LOCUS Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length  
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 SECRETAGOGUE RECEPTOR TYPE 1 homolog [Rattus norvegicus], full  
 insert sequence.  
 ACCESSION AK049671  
 VERSION AK049671.1 GI:26340405  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 Carninci,P. and Hayashizaki,Y.  
 High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 2  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
 Kono,H., Akiyama,J., Nishi,K., Kutsuna,T., Tashiro,H., Itoh,M.,  
 Sumi,N., Ishii,Y., Nakamura,S., Hazada,M., Nishine,T., Harada,A.,  
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
 Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the  
 PANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861  
 PUBMED 11076861  
 REFERENCE 5  
 The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 MEDLINE 12002000  
 PUBMED 12002000  
 REFERENCE 6  
 Adachi,J., Aizawa,K., Akimura,T., Aikawa,T., Bono,H., Carninci,P.,  
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M.,  
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T.,





Query Match	7.4%	Score 226.8	DB 10	Length 500
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Matches 315	Conservative 0	Mismatches 147	Indels 0	Gaps 0
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Db	39	CCCTCTTCCCGCGCCGCTGCTGGCGGGGCGGTCAAGACGACACTGGCTGGCGGCTCTTCGCG	98	
QY	1180	TGCGGGGTGAGCGGCAAGTGTGTGACCCGTATGCTGATCGGGCGCTTACCGGAGATGCGGA	1239	
Db	99	TGGGCATGCGGGGCGACCTGCTCAACCATGCTGGGAGTGTGCGCTTCCGGAGGTGGGTA	158	
QY	1240	CCACCATCAACTTATACCTGGGAGAGATGGCCGGTGCAGCACTACTCATCTGCTCGGGG	1299	
Db	159	CCACCATCAACTTATACCTGGGAGAGATGGCCGGTGCAGCACTACTCATCTGCTCGGA	218	
QY	1300	TGCGGTTGACCTGATACCGGCTCTGGCGGCTCGCGCCCTTGAGTGTGCGGCGCGCTCT	1359	
Db	219	TGCCCTTGACCTGATGCGGCTCTGGGATTAACGGCCCTGGAACTTGGGCGACCTGCTCT	278	
QY	1360	GCGCCCTGTCCTTACGTGGGCGGAGGCGTGCACCTTACGCGACGCTGTCACATGACCG	1419	
Db	279	GCAAACTTTCAGTTGTGACGAGAGGCTGACCTTACGCTACGCTGTACACATCACCG	338	
QY	1420	CGCTCAGCGTGCAGCGCTTACCTGGCCGATCTGCCCGCCGCTCCGCGCCGCGCTTGTGCA	1479	
Db	339	CGTGAAGGTGAGCGGTACTTGTGCGCATCTGCTTCCGCTGGCGGCGCAAGGTGATGCA	398	
QY	1480	CCCGGCGCGCGTCCGCGGCTATGCTGCTGCTGGGCGGCTGCTGCTCTCGCG	1539	
Db	399	CCAAAGGCGCGGTGACCTGCTATCTGTGATCTG3GCCGCTTCTGACGCGCG	458	
QY	1540	GTCCCTTCTGTTCTGCTGATGGGCGCTGCAGCAGACCCCGCA	1581	
Db	459	GGCCCATCTTCTGCTGCTGATGGAGATGAGATGAGATGGA	500	

RESULT 10	608 bp	mRNA	linear	EST 17-DEC-2002
BY724644	BY724644	RIKEN full-length enriched, 0 day neonate thymus Mus		
LOCUS	musculus cDNA clone M430103P18 5', mRNA sequence.			
DEFINITION	musculus cDNA clone M430103P18 5', mRNA sequence.			
ACCESSION	BY724644			
VERSION	BY724644.1	GI:27137769		
KEYWORDS	EST.			
SOURCE	Mus musculus			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognatha; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 608)			
	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishikido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, K. A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gotohori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kenakin, A., Mansude, H., Baralov, S., Beisel, K. W., Blake, C. A., Brad, D., Brusic, V., Chochina, C., Corbett, L. S., Cousins, S., Dalia, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guinacchia, S., Hirokawa, N., Jackson, I. D., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Leshar, B., Lyons, P. A., Magliotti, D. R., Matsuda, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numa, K., Okido, T., Pavan, W. O., Pettes, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sander, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takemaki, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Waterbury, J., Wells, C., Wilming, L. G., Wymshak-Boris, A., Yang, L., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Giannini, P.,			

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Best Local Similarity	70.3% Pred. No. 6.ee-17;
Matches 253; Conservative	0; Mismatches 124; Indels 0; Gaps 0
QY	1165 TGTGCTGTTCCTGCTCGGGGTGAGCCGCAACGTGTGACCGTGATGTCGAGCGCT 1224
DB	2 TGGCGCTCTGTGGTGGGCAATCTCGGGCAACCTGCTACCAATGCTGTGTGTCCCGCT 61
QY	1225 ACCGGGAACATGGAGCAACCAACCAACTTGTATCTGTGGGAGAGATGGCCGTCCGACATAC 1284
DB	62 TCCGGAGAGTGGCAACCAACCAACTCTTACTTACAGCATGAGGCTTCTCGAATCTGC 121
QY	1285 TCATCTCTGCTGGGCTGGCCCTTTCAGCTGTATACCGCTCTGCGCTCGCGCCCTGGAGT 1344
DB	122 TCATCTCTGCTGTGATGAGCCGTGAGCTCTGCTCGCCTGTGACATGTGCGCCCTGGAAT 181
QY	1345 TCGGGCGGCTCTGTCGCGCGCTGTCCTTAGTGTGGGAGAGGGCTGCACTTACGCGACAG 1404
DB	182 TCGGGGACCTGCTTGCMAACTCTTCCAGTTTGTACAGAGACTGCACTTACGCGACAG 241
QY	1405 TGCCTCACATGACCCGCGCTGACGCTGACGCGCTACCTGACCATCTGCCCGCGCTCCG 1464
DB	242 TCTCATCATGACCGCGCTGAGCTGACGCGCTACTTCCATCTGCTTCCGCGTGGG 301
QY	1465 CCGCGCTTGTGGTACCCGCGCGCGCGCTCCGCGCGCTACATCGCTGTGCTCTGGCGCGT 1524
DB	302 CCAAGTGTGTGTATACCAAGGCGCTGTGAGCTGTGATCTTGTGATTTGGGCTGTGG 361
QY	1525 CGCTGCTCTGCGCGCTCCCTCTTCTTCTCTGCTGGTGGCGCTGACAGAGACCCGCGCA 1581
DB	362 CCTTCTGACAGCGCGGCGCCCATCTTCTGCTGTGGTGGCGCTGAGACAGAACGCGCA 418
RESULT 11	
LOCUS	AY407665 969 bp DNA linear GSS 15-DEC-2003
DEFINITION	Pan troglodytes GHR gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION	AY407665
VERSION	AY407665.1
KEYWORDS	GI:39763636
SOURCE	GSS
ORGANISM	Pan troglodytes (chimpanzee)
REFERENCE	Pan troglodytes (chimpanzee)
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
TITLE	1 (bases 1 to 969)
TITLE	Clark,A.G., Glawoski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
JOURNAL	Direct Submission
COMMENT	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
FEATURES	This sequence was made by sequencing genomic exons and ordering them based on alignment.
source	Location/Qualifiers
gene	1..969
	/organism="Pan troglodytes"
	/mol_type="genomic DNA"
	/db_xref="taxon:9598"
	<1..-3969



/db\_xref="taxon:9606"  
 /clone="DKFZp341j320"  
 /tissue\_type="testis"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_id="434 (synonym: htes3)"  
 /note="Vector: pSPori1; Site\_1: NotI; Site\_2: SalI"

## ORIGIN

Query Match 6.5%; Score 200.8; DB 9; Length 489;  
 Best Local Similarity 77.9%; Pred. No. 1.1e-14;  
 Matches 268; Conservative 0; Mismatches 72; Indels 4; Gaps 2;

QY 2 TGAATATATCTGTCAGTCCGCGCGGCGCTCAGCGCTGTAATCCAGCACTTTGGG 61  
 Db 147 TGAATATCTGTCAGTCCGCGCGGCGCTCAGCGCTGTAATCCAGCACTTTGGG 206  
 QY 62 AGGTGAGCGCGGTGAGCACTTGGGCTCAGAGATTGAGACCAAGCTGGCCAACTGGC 121  
 Db 207 AAGCGAGCGAGGTGATCCTGAGGTGAGAGATTGAGACCAAGCTGGCCAACTGGT 266  
 QY 122 GAACCCCTGACTACACAAAAACAAATTTAGCCGCGGCTTGGGC---GCTTCCTGTC 178  
 Db 267 GAACCCCGCTCTTAACCTACAAATAATTAGCTGGGCGTGTGCGACAGCACTTGTGA 326  
 QY 179 TCCAGCTACTCAGAGGCTGAGGTGGAGAGACTGCTTGAAGCTGGAGGTCGAGCTGC 238  
 Db 327 TCCAGCTACTCAGAGGCTGAGGTGGAGAGATTGCTTGAAGCTGGAGGTCGAGCTGC 386  
 QY 239 AGTGAAGTGTATCGCGCACTTAACTCCAGCTGGAGACAGTGAAGACCTGTCTCAA 298  
 Db 387 AGTGAAGCAATATGCTCCA-TTGCACTCCAGCTGGGTGAGCACTGCAATCTCA 445  
 QY 299 GAAAGAAAAAGAAAGAAAGAAAGAAAAAGAAAAAGAAA 342  
 Db 446 AATTAAGATAAAGATATGTCTGCAAAAAAGAAAAA 489

## RESULT 14

BC035179 2669 bp mRNA linear HTC 04-MAR-2003  
 LOCUS BC035179  
 DEFINITION Homo sapiens, clone IMAGE:5266192, mRNA.  
 ACCESSION BC035179  
 VERSION BC035179.1 GI:23273366  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 2669)  
 Strausberg, R.  
 Direct Submission  
 Submitted (31-JUL-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki  
 Toshuyuki and Piero Carninci (RIKEN)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)  
 Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha  
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

## REMARK

## COMMENT

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/BLN.ac: <http://image.llnl.gov>  
 Series: IRAK Plate: 73 Row: c Column: 3  
 This clone has the following problem: retained intron.

## FEATURES

Location/Qualifiers  
 source 1..2669  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5266192"  
 /tissue\_type="testis"  
 /clone\_id="NIH MGC\_97"  
 /lab\_host="DH10B"  
 /note="Vector: pBlueScript"

## ORIGIN

Query Match 6.5%; Score 198.2; DB 11; Length 2669;  
 Best Local Similarity 68.2%; Pred. No. 1.2e-14;  
 Matches 305; Conservative 0; Mismatches 138; Indels 4; Gaps 2;

QY 2 TGAATATATCTGTCAGTCCGCGCGGCGCTGCTTACCGCTGTATCCAGCACTTTGGG 61  
 Db 1252 TAAAGCAATGAAACAGCTGGGCCAGTGGCTCAAGCTGTATCCAGCACTTTGGG 1311  
 QY 62 AGGTGAGCGCGGTGAGCACTTGGGCTCAGAGATTGAGACCAAGCTGGCCAACTGGC 121  
 Db 1312 AGGTGAGCGCGGTGAGTCACTGAGTCAAGAGTTTCAAGACCAAGCTGACCACTGGT 1371  
 QY 122 GAACCCCTGACTACACAAAAACAAATTTAGCCGCGG---GCTTGGCGCTTCTGTGC 178  
 Db 1372 GAACCCCGCTCTTCTTAAATACAAATTTAGCAAGTATGTCGACGCTGCTGTAA 1431  
 QY 179 TCCAGCTACTCAGAGGCTGAGGTGGAGAGACTGCTTGAAGCTGGAGGTCGAGGCTGC 238  
 Db 1432 TCCAGCTACTCAGAGGCTGAGGTGGAGAGATTGCTGGAACCTGGAGGTGGAGCTGC 1491  
 QY 239 AGTGAAGTGTATCGCGCACTTAACTCCAGCTGGAGACAGTGAAGACCTGTCTCAA 298  
 Db 1492 AGTGAAGCAATATGCTCCA-TTGCACTCCAGCTGGGTGAGCAAGCACTGATCAA 1550  
 QY 299 GAAAGAAAAAGAAAGAAAGAAAGAAAAAGAAAAAGAAATTTTGGTCAATTAT 358  
 Db 1551 AAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAAGAAAAAGAAAAAGAAATAGAAC 1610  
 QY 359 ATGTCAGCTCCCTCCACACTCGGAATTTACAGAAAGAGAACTGGGCTGGCGAGA 418  
 Db 1611 CAGGTGAGTGTCTTAACTTGGAGAAAGTATGTAGCAGCTTAAACAGGCAATGTGTAA 1670  
 QY 419 CCAGAGCTAGCCCAAGATTACCAAGT 445  
 Db 1671 TTGTTCAACTTGACACTACGAGGT 1697

## RESULT 15

BO778458 606 bp mRNA linear EST 26-JUL-2002  
 LOCUS BO778458  
 DEFINITION Homo sapiens CDNA clone IMAGE:6031548 3,  
 mRNA sequence.  
 ACCESSION BO778458  
 VERSION BO778458.1 GI:21986930  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 606)  
 Lemishka, I., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K.,  
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,  
 Schmitt, A., Theising, B., Ritzer, E., Roth, I., Bennett, V.,  
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, R.,  
 Williams, T., Jackson, Y., and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)

## REFERENCE

Other ESTs: 1131d07.y1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium

## TITLE

Unpublished (2000)  
 Other ESTs: 1131d07.y1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium

## JOURNAL

Unpublished (2000)  
 Other ESTs: 1131d07.y1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium

Unpublished (2000)  
 Other ESTs: 1131d07.y1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu  
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center for information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)  
Seq primer: -40UP from Gibco

High quality sequence stop: 450.

## FEATURES

## SOURCE

1..606  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6031548"  
/tissue\_type="Purified pancreatic islet"  
/lab\_host="DH10B"  
/clone\_id="HR85 islet"  
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
Size-selected on agarose gel. Average insert size ~1kb. 5'  
XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD,  
Metabolism Div. (Alan Permut Lab), Washington University  
School of Medicine, Box 8127, 660 South Euclid Ave., St.  
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
314-362-1916, Fax: 314-747-2692."

## ORIGIN

## Query Match

6.5%; Score 197.8; DB 13; Length 606;  
Best Local Similarity 78.2%; Pred. No. 2.3e-14;

Matches 251; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

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QY 20 GCCGGGCGGGTGGCTCAAGCCTGTATCCAGACATTGGAGGCGAGGGGTGGAC 79
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Db 191 GCCAGGACGGTGGCTCAAGCCTGTATCCAGACATTGGAGGCGAGGGGTGGAT 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 CACCTGGGGTCAAGAGTTGAGACCAAGCTGGCCACATGGCGAAACCTGACTACACAA 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 251 CACCTGAGGTCAGAGAGTTGAGACCAAGCTGGCCACATGGCGAAACCTGCTCTACTA 310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 140 AAAACACAAAATTAGCCGGG---GCTTGGGGCGCTCCTGTGCTGCCAGCTACTCAGGAGG 196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 311 AAAGTACAAAATTAGCTGGGTGTGTGTGGCGGGTGTCTGTATCCAGCTACTCAGGAGG 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 197 CTGAGGTGGAGGAGCTGCTTGAAGCTGGAGAGTGAAGGCTGACGTGATTCGGCGC 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 371 CTGAGGCGAGGAGACTGCTTGAACCTGGAGGCGAGGTTGCAGTGAAGTGAATTCGGC 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 257 CACTTAAGTCCAGCTGAGAGACAGTGAAGCCTGTCTCAAGAGAAAAAAGAAAGAA 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 431 CACTGCACTCAGCCTGGGCGACAAAGACAAAGTCAATCCAAAAAAGAAAAAAGAAAGAA 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 317 AGAAGAAAAAAGAAAAA 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 491 CAAAAACAAAAACAAAAAA 511
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Job time : 7454 secs

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